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Search time 1300.69 Seconds (without alignments) 253.213 Million cell updates/sec
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                                                                                                  ..tgatcggccgcaag
                                                                                                                                                          1598348
version 4.5
- 2000 Compugen Ltd.
                                                                                                                                                           hits satisfying chosen parameters:
                                                                                                                                          7991742 seqs, 3503743858 residues
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Maximum Match 100%
Listing first 45 summaries
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                                nucleic search, using sw model
                                                2001, 11:46:04
                                                                                                   agctataatgcggccgcata..
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GenCore
Copyright (c) 1993
                                                                          US-09-101-423B-8
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em_esthum1:*
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Maximum DB seq length: 200000000
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gb_est2: *

gb_est4: *

gb_est5: *

gb_est6: *

gb_est6: *

gb_est7: *

gb_est11: *

gb_est11: *

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gb_est12: *

gb_est11: *

gb_est21: *

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gb_est37:
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44: em_esthum2:*
45: em_esthum3:*
46: em_esthum3:*
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57: em_esthum11:*
60: em_esthum2:*
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em_estpl6:*
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A1283439 qh93e10.x
AA236621 zs43g09.r
AQ841408 T136718b
BE036773 MP05D02 M
AW977483 EST389592
BE062593 QV1-BT026
A1514427 LD40932.5
AA952587 TENS1771
AA063113 zf68e10.s
A1187524 EST316 Ma
BE535565 601059673
AV624476 AV624476
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AW181091 MGA0032r
AQ578848 nbxb0093F
AZ342872 1M0076E01
AW181091 MGA0032r
AQ578848 nbxb0093F
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AW181091 MGA0032r
AQ578848 nbxb00937
AX342872 1M0076E01
AW181091 MGA0032r
AQ578848 nbxb00937
AW426457 AV426457
AW330028 TENU4569
AV426457 AV426457
AW330028 TENU4569
AV426457 AV426457
AW330028 TENU4569
AV426457 AV422473
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AV426457 AV426457
AW33002 TENU4569
AV426457 AV426457
AW491371 UI-M-BH3-BE640770 Cri2_1_A1
AW91251 UI-M-BH3-BE943769 UI-M-BH3-BE943769 UI-M-BH3-BE943769 UI-M-BH1-AW14910 707013F10
BE647694 UI-M-BH1-AW14910 707013F10
                          Wo. is the number of results predicted by chance to have a preater than or equal to the score of the result being printed derived by analysis of the total score distribution.
                                               SUMMARIES
                                                                   18 A1283439
4 AA236621
163 AQ841408
134 BE036773
97 AW977483
134 BE062593
21 A1514427
14 AA952587
23 A1667900
1 AA063113
17 A1187524
109 BE535565
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107 BE363902
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143 N77089
143 AN144910
110 BE647694
gb_gss25:*
gb_gss26:*
gb_gss27:*
gb_gss28:*
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## ALIGNMENTS

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mRNA 23-NOV-1998 AI283439 313 bp mRNA EST 23-NOV-19 qh93e10.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1854570 3' similar to TR:P76904 P76904 SIMILAR TO ;, sequence. AI283439 AI283439.1 GI:3921672 EST. LOCUS DEFINITION ACCESSION VERSION KEYWORDS RESULT AI283439

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109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DH10B"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 520)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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                                          Euteleostomi;
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clone IMAGE:688000
                                                                                                                             oject (CGAP)
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                                          Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae
                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pr
                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL ; IMAGE Consortium (info@image.llnl.gov) for further Seq primer: -40UP from Gibco High quality sequence stop: 297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO
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                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1854570"
/clone_lib="Soares_NFL_T_GBC_S1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.8%; Score 23.4; Ilarity 73.2%; Pred. No. 31; Conservative 0; Mismatches
                                                                                                                                                Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 313)
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similar to '
AA236621
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SOURCE
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/db_xref="Taxon:9606"
/clone_lib="Soares_NhHMPu_S1"
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/lab_host="Dhilbs"
/note="Corgan: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_l: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQ841408 558 bp DNA GSS 27-SEP-1999
T136718b shotgun sub-library of BAC clone 16K14 Medicago truncatula
genomic clone 16-K-14-022, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatophyta;
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Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 618 Std Error: 0.00

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 425.
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Other name: BSC-19-22; date: 6/8/99; Submitted to the Database
Genome Survey Sequences (GSS) on 09/27/99; More information is
available at 'http://chrysie.tamu.edu/medicago'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Kim, D., Choi, H., Peng, H., Ellis, L. and Cook, DR.
BAC survey sequencing of Medicago truncatula (1999c)
Unpublished (1999)
Contact: Cook DR
The Crop Biotechnology Center
Texas A&M University
Department of Plant Pathology and Microbiology, Rm 120
Peterson Bldg, College Station, TX 77843-2132, USA
Tel: 409 845 8743
Fax: 409 862 4790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 520;
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Class: BAC subclone
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AQ841408.1
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Best Local Similarity
Matches 30; Conser
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Seg primer
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RESULT 5
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      /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/db_xref="taxon:3880"
/clone="16-K-14-022"
/clone_lib="shotgun sub-library of BAC clone 16K14"
/note="Vector: pUC18; BAC survey sequences were obtained from sheared BAC DNA subcloned into the Smal site of pUC18. The template DNA for sequencing was obtained by PCR using universal primers. Sequencing reactions were primed from the PUC-C primer site (CAGGAAACAGCTATGACTATACGA)
in the pUC18 polylinker."
                                                                                                          obtained by PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                             common ice plant.

Mesembryanthemum crystallinum

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;

Caryophyllales; Aizoaceae; Mesembryanthemum.

(bases 1 to 1054)

Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferrea, H., Kawasaki, S., McCollough, A., Michalowski, C.B., Palacio, C., Functional Genomics of Plant Stress Tolerance
Unpublished (2000)

Contact: Michalowski, C.B.

University of Arizona
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/db_xref="taxon:3544"
/clone_lib="MP"
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il: cbm@u.arizona.edu
t blastx match: 'emb|CAB38794.1| (AL035678) pu
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/dev_stage="6 weeks"
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llarity 70.5%;
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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AW977483 705 bp mRNA EST 02-JUN-2000
EST389592 MAGE resequences, MAGO Homo sapiens cDNA, mRNA sequence.
AW977483
                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 705)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Hol, 'I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE062593 528 bp mRNA EST 09-JUN-2000 QV1-BT0260-281099-023-c01 BT0260 Homo sapiens cDNA, mRNA sequence BE062593.1 GI:8407243
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Assessment of gene expression patterns in a model of metastasis using a 19,200 element cDNA microarray Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                   model of
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/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGO"
/note="Vector: pBluescriptSKm"
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Pred. No. 82;
0; Mismatches
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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Plate: 378
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larity 72.5%;
Conservative
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                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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/dev_stage="Adult"
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31 a 180 c 152 g 94 t 1 others
       Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV1-BT0260-281
099-023-c01&t3=1999-10-28&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 426.
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/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="XL1 Blue"
/note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2: XhoI; Sized fractionated cDNAs were directly ligated into
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Email: http://www.fruitfly.org/EST, est@fruitfly.b. Plate: 409 row: C column: 8

High quality sequence stop: 507.

Location/Qualifiers
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BDGP/HHMI Drosophila EST Project
Unpublished (1997)
Contact: Harvey, D.
G. M. Rubin-Molecular and Cell Biology
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/clone="LD40932"
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Pred. No. 96;
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Location/Qualifiers
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Drosophila melanogaster
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+55-11-2707001
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AI514427/C
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1. .267
/organism="Trypanosoma cruzi"
/strain="Cl-Brenner"
/db_xref="taxon:5693"
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/clone_1771"
/clone_11p="T. cruzi epimastigote"
/clone_1771"
/clone_11p="T. cruzi epimastigote"
/clone_1771"
/clo
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TENGO871 T. Cruzi epimastigote normalised cDNA Library Trypanosoma cruzi cDNA clone n442.r 5', mRNA sequence.
AI667900 AI667900.1 GI:4826272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i epimastigote normalized cDNA Library Trypanosoma 1771 5', mRNA sequence.
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Av. Gral Paz entre Albarellos y Constituyentes, INTI edificio cp(1650) San Martin, Prov. de BS AS. Argentina
Tel: (54-1)752-9639 or (54-1)752-0021
Fax: (54-1)752-0021 or (54-1)752-9639
Email: dsanchez@inti.gov.ar
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.

Trypanosoma; Schizotrypanum.

Verdun, R.E., Di Paolo, N.C., Urmenyi, T.P., Rondinelli, E., Fra, A.C.C. and Sanchez, D.O.
Gene discovery through expressed sequence tag sequencing in trypanosoma cruzi
Infect. Immun. 66 (11), 5393-5398 (1998)

Contact: Sanchez D.O.
Instituto de Investigaciones Biotecnologicas (Univ. Nac. de
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Pred. No. 1.1e+02
); Mismatches 1
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                                                                                                                                                                               Score 22.2; D
Pred. No. 97;
0; Mismatches
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llarity 73.7%;
Conservative
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TENS1771 T. cruzi
cruzi cDNA clone 1
AA952587
AA952587.1 GI:311
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166
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les 28; Conser
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Trypanosoma
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Similarity 28; Conser
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos.comin,
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
E 1 (bases 1 to 447)
S Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins
,M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E.,
No. Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E.,
Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                             Unpublished (1998)
Contact: Delgado Alberto
Contact: Delgado Alberto
Departamento de Biologia Molecular, Lab 303
Instituto de Parasitologia y Biomedicina
Consejo Superior de Investigaciones Cientificas C/ Ventanilla No 11
, E-18001, Granada, Spain
Tel: 34 958 805058
Fax: 34 958 203323
Similar to T.cruzi elongation factor 1-gamma (mammalian homologue)
mRNA, gb|L17307|TRBEF1GHOM with Blastn.
Seq primer: T7
High quality sequence stop: 313.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA063113 447 bp mRNA
zf68e10.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone
IMAGE:382122 3' similar to contains element LTR5 repetitive element
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Site_1: EcoRI; Site_2: NotI; cDNA library constructed with oligo dt primed epimastigote mRNA and cloned in pt7t318D phagemid with modified polylinker" 91 c 83 g 67 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                         Gonzalez Rey, E., Remisz, E., Delgado Garcia, A. and Gonzalez, A. Characterization of ESTs from Trypanosoma cruzi epimastigotes
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                                                                 Trypanosomati
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larity 73.7%; Pred. No. 1.1e+02;
Conservative 0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218 AGTACTGCCGCAACTGCAGCCCGTGCGGCCGCAAGCTT 255
                                       Trypanosoma cruzi
Eukaryota; Euglenozoa; Kinetoplastida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Trypanosoma cruzi"
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/db_xref="taxon:5693"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="T. Cruzi epim
/cell_type="epimastigote"
/note="Site_1: EcoRI; Sit.
constructed with oligo dt
                                                                                   Trypanosoma; Schizotrypanum.

1 (bases 1 to 313)
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0
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                       Trypanosoma cruzi.
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AA063113
AA063113.1 GI:15
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les 28; Conserv
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KEYWORDS
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Diversity of odourant binding proteins revealed by an expressed
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information Insert Length: 826 Std Error: 0.00 Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Dit; Sphingiodea; Sphingidae; Sphinginae; Manduca.
1 (bases 1 to 475)
Robertson, H.M., Martos, R., Sears, C., Todres, E.2., Walden, K.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Manduca sexta"
/db_xref="taxon:7130"
/clone="pMsmaD85"
/clone_lib="Manduca sexta male antennae Uni-ZAP XR
library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence tag project on male Manduca sexta moth antennae Insect Mol. Biol. 8, 501-518 (1999)
Other_ESTS: EST315
Contact: Robertson HM
Department of Entomology
University of Illinois at Urbana-Champaign
505 S. Goodwin, Urbana, IL 61801, USA
Tel: 217 333-0489
Fax: 217 244 3499
Email: hughrobe@uiuc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 others
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Pred. No. 1.1e+02;
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Insert Length: 1000 Std Error: 0.00
Seq primer: T7
High quality sequence stop: 300.
Location/Qualifiers
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                                                                                                                                        /organism="Homo sapiens"
/db_xref="GDB:1290379"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                         M.Fatima Bonaldo. 104 c 114 g
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70.0%;
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/dev_stage="newly eclosed adults and pharate adults"
/lab_host="XL1 Blue MRF and SOLR"
/lab_host="XL1 Blue MRF and SOLR"
/note="Organ: antennae; Vector: Uni-ZAP XR; Site_1: ECORI;
Site_2: XhoI; The library was prepared by Stratagene using
oligo-T priming and unidirectional cloning with an
adaptor at the 5' end (GGCACGAG) following the EcoRI
site. The mRNA was prepared from antennae of late pupal
and newly eclosed male moths. Clones were subcloned in
vivo in mass into pBluescript maintained in SOLR cells
for DNA sequencing."
111 c 172 g 87 t
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Primer: Oligo dT.
ared by Life
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 892)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                       Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Site_2: Sall; Cloned unidirectionally. Pr
Average insert size 1.5 kb. Library prepara
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Pred. No. 1.2e+02;
); Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                         Score 22; DB 17;
Pred. No. 1.1e+02
); Mismatches 1
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High quality sequence stop: 612.
Location/Qualifiers
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/clone_lib="NIH_MGC_10"
/cell_line="MGC36"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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illarity 67.4%;
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nilarity 73.7%;
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BE535565
BE535565.1 GI:
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Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
Chlamydomonadaceae; Chlamydomonas.
S Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Nakamura, Y. and Tabata, S.
Generation of Expressed Sequence Tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
DNA Res. (2000) In press
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Chlamydomonas reinhardtii 5% to 0.04% CO2"
/clone_lib="Chlamydomonas reinhardtii 5% to 0.04% CO2"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from cells cultured
in a carbon stress acclimatized condition in which carbon
dioxide concentration in the bubbling gas was changed from
5% to 0.04%"
157 c 116 g 94 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ342872 558 bp DNA GSS 29-SEP-2000 1M0076E01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0076E01 F, DNA sequence. AZ342872 AZ342872.1 GI:10420544 GSS.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 558)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                  EST 11-OCT-2000
5% to 0.04% CO2 Chlamydomonas
', mRNA sequence.
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/organism="Chlamydomonas reinhardtii"
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Pred. No. 1.4e+02,
); Mismatches
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AV624476 Chlamydomonas reinhardtii
reinhardtii cDNA clone LC078c03_r 5
AV624476
AV624476.1 GI:10773653
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/db_xref="taxon:3055"
/clone="LC078c03_r"
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Contact: Robert B. Weiss
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Matches

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IACR-Long Ashton Research

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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PwD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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田
                                                                        Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: E column: 01
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 558.
Location/Qualifiers
1. 558
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0076E01"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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Mycosphaerella graminicola
Eukaryota; Fungi; Ascomycota; Ascomycota incertae sedis;
Mycosphaerellaceae; Mycosphaerella.

1 (bases 1 to 610)
Keon, J.P.R., Bailey, A.M. and Hargreaves, J.A.
A group of expressed cDNA sequences from the wheat fungal blotch pathogen, Mycosphaerella graminicola
Unpublished (1999)
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research
84112, USA
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/lab_host="E.
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Cell Biol
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Long Ashton, Bristol, BS41 9AF, UK
Tel: +44(0)1275 392181
Fax: +44(0
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## SUMMARIES

	Description	ŀ	DNA CAG. Syntheti	Hamster oral papil	Hamster oral papil	Primer HUCKN.NOT f	T. gondii immunoge	Semaphorin K1 gene	DNA sequence of so	Nucleotide sequenc	Stealth virus nucl	Olfactory receptor	Lambda INNER prime	Sequence encoding
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Matches 29;
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                                                                                                     A DNA tag (T72784) having HindIII, SfiI, NotI and a defective
C HindIII site is used to tag human DNA from malignant, metastatic
C cancer cells in a novel method of screening and recovering
C metastasis-inducing DNA (Met-DNA). This method involves
C transferring the human DNA into a cell line (pref. rat Rama 37)
C that produces only benign, non-metastasing tumours when injected
C into a syngeneic animal, injecting the transformed cells into a
C syngeneic animal, selecting those animals having metastasing
C tumours, and recovering the Met-DNA (see also T72785-90) from them.
C The human DNA is tagged to assist in its removal or insertion from
C or into a host or vector. The tagging procedure overcomes the
C problem of identifying the inserted human DNA sequences in the rat
C genome of the transfected cells.
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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ss.
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                              metastasis-inducing DNA - used to develop products treat patients at risk from metastatic tumours
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                                                                                                                                                                                                                                                                                                                                                                                Length 45;
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treatment;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 45 BP; 11 A; 13 C; 12 G; 9 T; 0 other;
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4e-08;
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P-PSDB; W47224.
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                             New isolated identify and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for,
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                                                                                                                                                                                                                                                                                                                    Diagnosis; papilloma virus infectious disease; cancer; screening; antitumour agent; antisense treatment;
                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a hamster oral papilloma virus gone. The DNA can be used for the diagnosis of papilloma infectious diseases related to cancer, screening for antagents and antisense treatment.
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 DB 19;
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Score 21.8; D) Pred. No. 9.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 21.8; DF
Pred. No. 12;
0; Mismatches
                 ed. No. 9.9, Mismatches
                                                                                                                                                                                                                                                                                    oral papilloma virus genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Pages 14-16; 17pp; Japanese.
                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                               RESULT 3
V15519/c
ID V15519 standard; DNA; 7647 BP
                                                                                                                                                                                                                                                                                                                                                                   Hamster oral papilloma virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96JP-0207143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.4%;
llarity 70.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96JP-0207143.
46.48;
70.78;
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                                                                                                                                                                                                                                                    (first entry)
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                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TORA ) TORAY IND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-186869/17
               Local Similarity
les 29; Conser'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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Sequence 1818 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunogens
                                                                                                                                                                                                                                          26;
                                                                                                                                                                                                                      Query Match
Best Local 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              purposes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                         246842;
                                                                                                                                                                                                                                                                                                                                                  Z46842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New
                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                        Z46842
                                                                                                                                                                                                                                                                                                                                                                                                                                 Db
X F F X S X O O O O O O O O X S O S
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic protein; Toxoplasma gondii protein; oocyst shedding; cat;
T. gondii infection; enteric apicomplexa oocyst; Cryptosporidium oocyst;
Toxoplasma oocyst; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                       cDNA encoding an immunoglobulin (Ig), light chain, constant region. The primer can be used in a novel method for the production of recombinant antibodies, comprising the selection of B cells from a lymphocyte fraction, isolation of mRNA from individual B cells, reverse transcription of the mRNA into cDNA, amplification of the cDNA by PCR and cloning and expression of the cDNA. The recombinant antibodies can be used for diagnosis and/or therapy, while the method avoids the need for intermediate separation of light and
                                                                                                                                                                                                                                           of the
                                                                                                                                                                                     and
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                                                                                                                                                                                     bu.
                                                                                                                                                                                                                                                                                                                                                                                                           42;
                                                                                                                                                                                                                                              present sequence is a primer for the PCR amplification
                                                                                                                                                                                     cloni
                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                  Prodn. of recombinant antibodies - by amplification, expression of cDNA generated from B-cell mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                            DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        45
                                                                                                                                                                                                                                                                                                                                                                         Sequence 42 BP; 11 A; 11 C; 14 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 6
                                                                                                                                                                                                                                                                                                                                                                                                           Score 21.4; D
Pred. No. 8.9;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gondii immunogenic protein encoding DNA
                                                                                                                                                                                                                                                                                                                                                   heavy chains and gene library screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                      Claim 5; Page 11; 11pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; DNA; 500 BP
                                                                                           95DE-1026546.
                                                                    95DE-1026546.
                                                                                                                                                                                                                                                                                                                                                                                                            45.5%;
71.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0994825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Milhausen MJ,
                                                                                                                                       Welschof
                                                                                                                                                              WPI; 1997-088250/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-418930/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                       . Similarity 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toxoplasma gondii
                      DE19526546-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HESK-) HESKA
                                                                                                                (OPEL/) OPELZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9932633-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-1998;
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                                                                                           20-JUL-1995;
                                                                   20-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1999
                                             23-JAN-1997
                                                                                                                                       Ъ,
Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lutz SB,
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                         Terness
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X91235
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X91235
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The invention provided isolated human semaphorin K1 polypeptides. The polypeptides, or nucleic acids encoding them, can be used to modulate cellular physiology by modulating semaphorin K1 activity, e.g. semaphorin K1 polypeptide fragments or antisense nucleic acids can be used to enhance neurite outgrowth from damaged neurons. The polypeptides can also be used as immunogens, reagents for isolating other semaphorins, or as reagents for screening chemical libraries for lead pharmaceutical agents. The nucleic acids can also be used as probes and primers for diagnostic
                                                                                                                                     encode immunogenic polypeptides. The T. gondii nucleic acid molecules, immunogenic proteins and antibodies to the proteins can be used to inhibit T. gondii oocyst shedding in a cat due to infection with T. gondii. They can be used for preventing T. gondii infection and for preventing the spread of T. gondii infection. They can also be used for detecting T. gondii infection. The detection method can be used to detect parasite cysts or oocysts in feces, e.g. from enteric apicomplexa oocysts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   physiology; neurite outgrowth; neuron; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                   that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful cell physiology modulators and
                                                                                                                provides isolated Toxoplasma gondii nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
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to
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    e.g.
                                                                                                                                                                                                                                                                                   parasite cysts or oocysts in feces, e.g. from enteric a such as Cryptosporidium oocysts and Toxoplasma oocysts.
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  acids used,
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                                                                                                                                                                                                                                                                                                                                                       Sequence 500 BP; 118 A; 118 C; 131 G; 133 T;
                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       473
                                                                                                                                                                                                                                                                                                                                                                                                            21.2; L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57pp; Japanese
 gondii nucleic
                          infection caused by this microorganism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
                                                                      Claim 4; Page 213; 381pp; English.
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(3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     semaphorin polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0041236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; cDNA; 1818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-0065672
                                                                                                                                                                                                                                                                                                                                                                                                                             45.1%;
ilarity 76.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EXEL-) EXELIXIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunogen; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 17-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Semaphorin K1; cellular
    Toxoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-109378/10.
B; Y56855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                    invention
  isolated
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                      Gaps
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                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_type= inverted
/note= "inverted repeat sequence IR1 as possible
transcription terminator for ORF2 gene as
indicated in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_type= inverted
/rpt_type= inverted repeat sequence IR2 as possible
/note= "inverted repeat sequence IR2 as possible
    transcription terminator for SLDH gene as
    indicated in the specification"
                    0;
  Length 1818;
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                                                                                                                                                                                                                                                                                                                                                      Ç
                                                                                                                                                                    of sorbitol dehydrogenase (SLDH) and ORF2 genes.
                                                                                                                                                                                                                                                                                                                        shown
                                                                                                                                                                                       dehydrogenase; SLDH; open reading frame; ORF2; L-sol; vitamin C; ds.
                                                                                                                                                                                                                                                                  "putative Shine-Dalgarno (SD) sequen
ORF2 gene"
                                                                                                                                                                                                                                                                                                                                                      sednen
                     Indels
                                                                                                                                                                                                                                                                                                                                                                                      /product= "SLDH gene product"
/note= "corresponding protein sequence
                                                                                                                                                                                                                                                                                                                        sedneuce
                                                                                                                                                                                                                                                                                                                                                                                                                                                            "mature SLDH protein sequence"
                                                                                                                                                                                                                                                                                                                                               /note= "putative Shine-Dalgarno (SD)
SLDH gene"
                                     'note= "signal sequence for SLDH"
  21;
                                                                                                                                                                                                                                                                                                            'product= "ORF2 gene product"
  DB
Score 21.2; D
Pred. No. 17;
0; Mismatches
                                                                                                                                                                                                                                       Location/Qualifiers
177..182
                   ö
45.1%;
69.0%;
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/rr+
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                                                                                                          standard; DNA; 3481
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/*tag= j
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                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                    Gluconobacter suboxydans.
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558..564
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                    Conservative
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         Similarity
29; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                    DNA sequence
                                                                                                                                                 21-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-AUG-1998;
                                                                                                                                                                                                -sorbitol;
                                                                                                                                                                                                                                                                                                                                                                                                             sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_unit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-AUG-1997
Query Match
Best Local
                                                                                                                                                                                       Sorbitol
                                                                                                          X21501
                                                                                       7
                    Matches
                                                                                                                                                                                                                                       Key
RBS
                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                               RBS
                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                      RESULT
X21501
                                                                                                                                                         XX
XX
XX
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XX
XX
YX
YX
YX
YX
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a protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sorbitol dehydrogenase (SLDH) activity. The DNA also encodes an open reading frame, needed for SLDH activity in vivo. Host cells transformed by a vector comprising the SLDH DNA sequence are used for the recombinant expression of the sorbitol dehydrogenase. Recombinant D-sorbitol dehydrogenase is useful for producing L-sorbose from D-sorbitol. L-sorbose is an important intermediate in vitamin C production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prototype Stealth virus clone; atypically structured virus; vacuolating cytopathic effect; cytopathic virus; virus detection; malignancy; multiple myeloma; lymphoma; brain tumour; breast cancer; salivary gland tumour; Alzheimer's disease; Parkinson's disease; spongiform encephalopathy; multiple sclerosis; schizophrenia; manic depression; major depression; personality disorder; autism; Rett's syndrome; attention deficit; oppositional defiance; aggression; anorexia nervosa; bulimia; multi-system illness; virus infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used to develop products for detection, prevention stealth virus infections -

    useful

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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene encoding
                                                                                                                                                                                                                                                                                                                                                          intermediate in vitamin C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0 other;
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                                                                                                    Tomiyama
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence of the SLDH
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                                                                                                 Shinjoh M,
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clones. The sequences illustrate the type of sequences that can be used to generate probes and to predict antigenic and biologically active products obtainable from a viral isolate, in the methods of the invention. The specification describes tissue culture, serological and molecular based methods to detect atypically structured viruses, such as Stealth viruses, which are able to induce a vacuolating cytopathic effect (CPE) in tissue culture, and are distinguishable from known cytopathic viruses, by appearance progression and/or host range, or by serological, electron microscopic and/or molecular markers. The products can be used for detecting viruses in patients with diseases such as a malignancy, e.g. multiple myeloma, lymphoma, brain tumours, breast cancer, salivary gland tumours, Alzheimer's disease, spongiform encephalopathy, multiple sclerosis, schizophrenia, manic depression, major depression, personality disorders, autism, Rett's syndrome, attention deficit, oppositional defiance, aggression, anorexia nervosa, bulimia, a multi-system
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This sequence represents a Stealth virus nucleic acid clone. The invention relates to a method of detecting and characterising a stealth virus by reacting a sample suspected of containing a stealth virus with a probe from a known stealth virus and sequencing the resultant isolated nucleotide. The method comprises the steps of: (a) isolating DNA or RNA from a sample suspected of containing a stealth virus, e.g. a culture of from a sample suspected of containing a stealth virus, e.g. a culture of cells showing a viral cytopathic effect; (b) testing the reactivity of the isolated DNA or RNA with a molecular probe that contains at least 18 or more contiguous nucleotides identical to sequence previously identified from a stealth virus; and, optionally (c) sequencing the isolated DNA or RNA molecules that react with the probe. The method is used to detect stealth virus in a biological product, food or in the environment. The method is also used to evaluate agents for their inhibitory or stimulatory effects on stealth virus replication and to determine capacity of the virus to recombine with and potentially alter
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Ten new olfactory receptor proteins and their biallelic markers have been described. The sequences encoding these receptor proteins and which contain the biallelic markers can be used for genotyping. The olfactory receptor proteins can be used to screen for substances which bind to them. See GENESEQ records 293816-25 and Y83386-95.
                                                                                                                                                                                                                                                                                                                                                                              Sequence 144460 BP; 46068 A; 27088 C; 26615 G; 44676 T; 13 other;
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                                                                                                                                                                                                                                New nucleic acids encoding ten different olfactory receptor and their biallelic markers, are useful in genetic analysis screening for compounds which bind to the receptor proteins
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                                                                     complementary to the lambda DNA sequence adjacent to the cloning for the cDNA insertions (see Q70113-14). In addition, primers we designed which were complementary to the plus strand of the most region of the EK coding sequence (see Q70115-16). Subcloning and sequencing provided a 116 amino acid EK heavy chain. This prote contained regions corresp. to tryptic peptides (see R57295-9).
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New nucleic acid encoding enterokinase activity - and rela
vectors, host cells, expression products and antibodies ar
useful in treating digestive disorders and for cleaving fu
                                                                 oligonucleotide primers were synthesised which were
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                                                                                                                                                                                                                                                                                                                            Sequence encoding Mycobacterium tuberculosis 540 and
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                                                                                                                                                                   DB 15;
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Best Local Similarity 71.1%; Pred. No. 22;
Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (3948..2395)
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/label=540 AA protein
/note="P81351"
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/label=517 AA protein
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252..1874
                                                                                                                                                                                                                                                                                                                                                        vaccine;
                                               50pp; English.
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87US-0019529
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                                                                                                                                        BP; 12 A; 10 C;
                                                                                                                                                                                                                                                                                                                                                        Diagnosis; assay; M.bovis;
                                                                                                                                                                                                                                                                       4260
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P-PSDB; P81351, P81868
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                                                                                                                                                                                                                                                                      N81768 standard; DNA;
                                               6; Page 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-FEB-1988;
06-FEB-1987;
                                                                                                                                         Sequence 41
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                    useful in
proteins
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N81768
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sequence that corresponds to the sequence represented by position 3950 to about 2390 and from position 3948 through position 2398 of N81768 is claimed. Also claimed is a peptide sequence that consists of a 5-40 AA residue sequence that corresponds to a sequence of the 540 AA residue protein (P81351) or the 517 AA residue protein (P81868) coded for by the DNA sequence. The proteins can be used for determining previous immunological exposure of a mammal to M.tuberculosis or M.bovis and for producing a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The gene was isolated by probing a lambda gtll expression library of M.tuberculosis DNA with monoclonal antibodies directed against M.tuberculosis-specific antigens. The 19kD, 71kD and the 65kD proteins and genes are claimed, and so is a vaccine comprising DNA encoding M.tuberculosis protein in a recombinant vaccine vector. P80216 is encoded on the complementary strand.
                                                                                                                                                                                                                                                                                                                                       Gaps
nucleotide
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 of the
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Pred. No. 39;
0; Mismatches
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                                                                                                                                                                                                                          Sequence 4260 BP; 733 A; 1332 C; 1481 G;
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consists
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192..1874
/*tag= a
complement (2398..41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 8; 82pp; English.
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                                                                                                                                                                                                                                                                                           Similarity 80.0%;
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 isolated DNA molecule
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NR: P80215, P80216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; DNA;
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It represents a novel use for the known Mt Hsp65 gene.

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The antigen of step (a) is selected from collagen, Mt Hsp65, myelin basic protein, myelin oligodenfocyte glycoprotein, protein, and epitopes thereof. These antigens mitigate cytotoxic responses and elicit antigen desensitisation. The method is used especially for treating rheumatoid arthritis or multiple
                                                          Gaps
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       Length 438
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis 65 kDa heat shock protein gene.
                                                       Indels
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        DB
Score 20.4; D
Pred. No. 40;
0; Mismatches
                                                                                                Example 2; Page 55-59; 72pp; English.
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96US-0019100.
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                          Similarity
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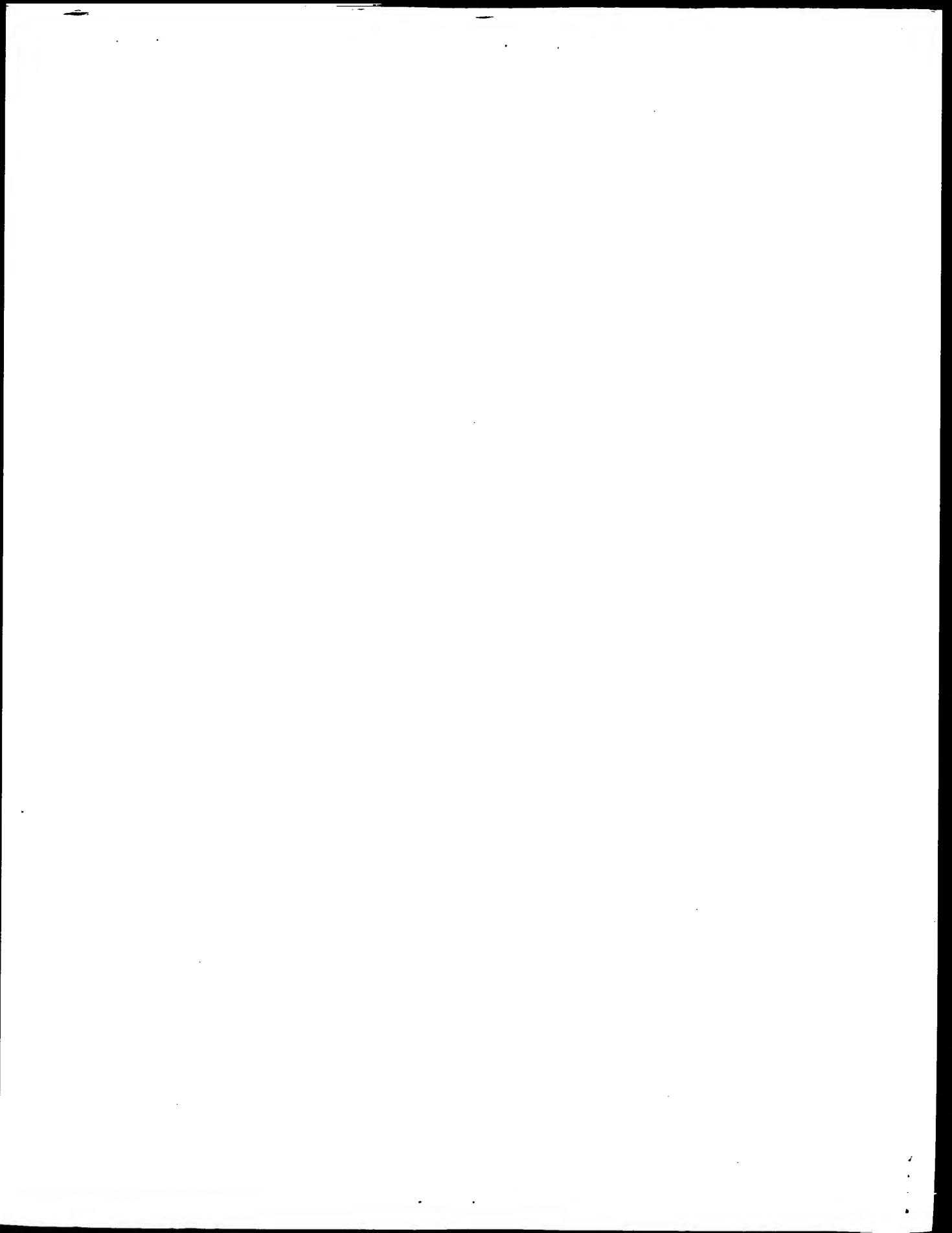
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and lung cancer.
                                                                                                                                                                                                                                                                                    Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
                                                                                   Gaps
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                        other;
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                       C; 1514
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Pred.
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                       A; 1371
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97US-0896164.
97US-0061599.
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                                                                                                                                                                                                                                                               associated gene
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                                                         43.4%;
llarity 80.0%;
Conservative
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Sahin
                       757
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                       Sequence 4380 BP;
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solated using
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17-JUL-1997;
10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
                                                                                                                                                                                                                                                              Colon cancer
                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                           WO9904265-A2
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                                                           Match
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Best Local Similarity 75.8%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 8;

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Search completed: March 4, 2001, 12:07:09 Job time: 5664 sec



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4, 2001, 12:05:17; Search time 106.76 Seconds (without alignments) 70.949 Million cell updates/sec
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    /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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    /cgn2_6/ptodata/2/ina/6_COMB.seq:*
    /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
    /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
    /cgn2_6/ptodata/2/ina/backfiles1.seq:*
GenCore version 4.5
(c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                  280836 segs, 80580151 residues
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Maximum Match 100%
Listing first 45 summaries
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47
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## SUMMARIES

	Description	Sequence 1, Ap	equence 26, App	equence 26, App	equence 2, Appl	equence 1, Appl	equence 5, Appl	equence 1, Appl	equence 7, Appl	equence 1, Appl	equence 1, Appl	equence 28, App	equence 6, Appl	equence 9, Appl	e 64, App	equence 67, App	equence 2, Appl	equence 3, Appl	equence 60, App	equence 61, App	equence 19, App	equence 3, Appl	equence 2, Appl	equence 1, Appl	equence 9, Appl	equence 3, Appl	equence 3, Appl	ence 1, Appl	equence 1, Appl
	ΠD	US-09-136-251-1	S-08-200-900	T-US94-00616-2	S-08-948-70	-08-054-077C	-629-643A-	-09-280-799-	-08-042-74	3-08-469-667-	-CT-US95-07289-	S-08-853-659A-	S-08-853-659A-	S-08-853-659A-	-08-853-659A-6	S-08-853-659A-	S-08-853-659A-	S-08-853-659A-	S-08-853-659A-	S-08-853-659A-6	S-09-320-878-1	CT-US95-02481-	S-08-576-626A-	S-09-335-40	S-08-278-630A	S-08-403-634-	S-08-913-4	-229	-08-516-801-
	DB	m	1	4	m	Н	٣	m	Н	Н	4	N	~	~	7	7	7	7	7	7	m	4	7	ო	<del>, ,</del>	<del>- 1</del>	က	က	7
	Length	348	4	4	88	4.1	72	72	94	63	63	79	96	96	96	968	470	470	70	470	850	170	802	75	37	42	42	1584	86
#P	Query Match	45.1	~	<u>~</u>	۳.	~;	~i	~;		<u>.</u>	ċ	<u>.</u>	<u>.</u>	<u>.</u>	Ċ	Ċ	Ċ	Ö	Ö	ö	ö	თ.	σ.	ص	ä	ω.	æ	æ.	ά.
	ore	21.2	0	0	0	φ.	<u>о</u>	<u>ი</u>	6	-	Н	ω.	ω.	80	8	ω.	ъ.	8	œ.	φ.	ω.	ω.	8	φ.	œ	œ.	œ.	•	œ.
	Result No.	-	2	m	C 4		φ				7	7	7	-	c 14	Н	c 16	П	c 18	7	C)	21	N	N	c 24	(A	.,	11	28

Sequence 1, Appli Sequence 9, Appli Sequence 13, Appli Sequence 1, Appli Sequence 10, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli Sequence 1, Appli	•	Length 3481; Indels 0; Gaps 0;  METHOD OF USE ffairs
29 18.2 38.7 1867 4 PCT-US95-06683-1  c 30 18.2 38.7 1965 1 US-08-258-420-9  c 31 18.2 38.7 2001 3 US-08-850-961-13  c 32 18.2 38.7 6028 3 US-09-011-745-5  33 18 38.3 1194 4 PCT-US94-09700-10  35 18 38.3 1134 4 PCT-US94-09700-10  36 18 38.3 1335 2 US-08-985-090-3  37 18 38.3 1335 3 US-09-165-543-3  38 18 38.3 1721 1 US-08-241-766-3  40 18 38.3 2100 1 US-07-970-462A-1  41 18 38.3 2106 4 PCT-US92-10904-1  42 18 38.3 2121 1 US-08-574-043A-1  44 18 38.3 2121 2 US-08-75-015-1  45 18 38.3 2121 2 US-08-795-015-1	RESULT 1  US-09-136-251-1  ; Sequence 1, Application US/09136251A ; Patent No. 6127156 ; GENERAL INFORMATION: ; APPLICANT: HOSHINO, Tatsuo ; APPLICANT: OJIMA, Setsuko ; APPLICANT: SHINJOH, Masako ; APPLICANT: SHINJOH, Masako ; APPLICANT: TOMIXAMA, No. 6127156ibumi ; TITLE OF INVENTION: D-SORBITOL DEHYDROGENASE GENE ; FILE REFERENCE: D-Sorbital Dehydrogenase Gene ; CURRENT APPLICATION NUMBER: US/09/136,251A ; EARLIER APPLICATION NUMBER: EP 97114432.4 ; EARLIER FILING DATE: 1998-08-21 ; NUMBER OF SEO ID NOS: 9 ; SOFTWARE: PatentIn Ver: 2.1 ; SEQ ID NO 1 ; LENGTH: 3481 ; TYPE: DNA ; ORGANISM: Gluconobacter suboxydans US-09-136-251-1	Query Match Best Local Similarity 76.5%; Pred. No. 10; Matches 26; Conservative 0; Mismatches 8;  Qy 13 gccgcatattcggcctgatcggccgcaagcttgg 46

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mat peptide
                                                                                                                                                                                                     ; ORGANISM: Homo Sapiens
US-08-948-705-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: SistoPOLOGY: linear
                                                                                                                                                                                                                                                                         Similarity
25; Conser
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STREET: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: M
                                                                                                                                                                 NO 2
                                                                                                                                                                                           TYPE: DNA
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Best Local 3
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                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                  SEQ ID
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                           (EPO)
             SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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Pred. No. 11;
0; Mismatches
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Pred. No. 1
                                                                                                                                   GI 5201-FWC
                                                    US/08/200,900A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT/US94/00616
                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Meinert, Maureen C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI 5201-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170 x8574
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26, Application PC/TUS9400616 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-948-705-2/c; Sequence 2, Application US/08948705A; Patent No. 6043084; GENERAL INFORMATION:
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0
PC compatible
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                                                             23-FEB-1994
N: 435
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71.18;
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Similarity 71.1%;
27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 2'
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
LENGTH: 41 base pairs
""PE: nucleic acid
                                   RRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 23-FEB-19
                                                                                                                                                                                                                LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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          OPERATING SYSTEM:
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                                                                              CLASSIFICATION:
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S-08-200-900A-26
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PCT-US94-00616-26
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                          SOFTWARE:
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Best Local
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Best Local (
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APPLICANT: Scanlan, Matthew J.

APPLICANT: Chen, Yao-Tseng
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Old, Lloyd J.

TITLE OF INVENTION: ISOLATED WITH COLON CANCER AND METHODS FOR DIAGNOSING AND
TITLE OF INVENTION: TREATING COLON CANCER
FILE REFERENCE: LUD-5506-JEL/NDH
CURRENT APPLICATION NUMBER: US/08/948,705A
CURRENT FILING DATE: 1997-10-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 SUBUNIT PROTEIN
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/054,077C
FILING DATE: 27-APR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     8;
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Patent No. 5527679
GENERAL INFORMATION:
APPLICANT: HEMLER, MARTIN E.
APPLICANT: RAMASWAMY, HEMAVATHI
APPLICANT: RAMASWAMY, HEMAVATHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 01-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-054-077C-1
; Sequence 1, Application US/08054077C
: Patent No. 5527679
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REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3415 base pairs
                                                                                                                                                                                                                                                                                                                                                                                           43.0%;
illarity 75.8%;
Conservative
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CORRESPONDENCE ADDRESS:
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                                                                                     DB 1;
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                                                                                                                                      8 atgoggcogcatattoggcotgatoggcogcaagcttgg
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Pred. No. 39;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                    Lundberg, Woessner
                                                                                    Score 19.8; D
Pred. No. 35;
0; Mismatches
                                                                                                                                                                                                                                                                                               TRANSGENIC MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 150.167WO1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-359-3260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/629,643A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/629,643
FILING DATE: 09-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Viksnins, Ann S
                                                                                                                                                                                                                              Sequence 5, Application US/08629643A Patent No. 6025539
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
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illarity 63.8%;
Conservative (
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                                                                                    42.1%;
illarity 69.2%;
Conservative
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomic DNA
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nucleic acid
EDNESS: single
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US-08-629-643A-5
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                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                    APPLICANT: Lee, J. L. APPLICANT: Lee, N. A. TITLE OF INVENTION: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    800
406..2733
                                     .2733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Schwegr
STREET: P. O. Box
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 30; Conser
                                                                                                 Local Similarity
nes 27; Conserv
                                                                                                                                                                                                                                       Patent No. 6025539
GENERAL INFORMATION:
APPLICANT: Lee, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: CLASSIFICATION:
                         337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                       USA
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           ; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-054-077C-1
                                                                                                                                                                                                      RESULT 6
US-08-629-643A-5
LOCATION:
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CITY: N
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                                                                                    Query Match
Best Local S
Matches 27
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                           Sequence 1, Application US/09280799
Patent No. 6136603
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Karras, James G
APPLICANT: MCKay, Robert
TITLE OF INVENTION: TRANSDUCTION
                                                                                                                                                                                                                                                                                                                                                                                      Length
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Sequence 7, Application US/08042747A

Patent No. 5487969

GENERAL INFORMATION:

APPLICANT: Eberle, Richard

APPLICANT: Black, Darla

APPLICANT: Hilliard, Julia K.

TITLE OF INVENTION: Cloning and Amplification of Mor

TITLE OF INVENTION: Virus Genes

NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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San Antonio
                                                                                                                                                                                                                                                                                                                                                                                  Score 19.8; D. Pred. No. 39; 0; Mismatches
                                                                                                                                                                     FILE REFERENCE: ISPH-0340
CURRENT APPLICATION NUMBER: US/09/280,799
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 208
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Haymond, W. Bradley
REGISTRATION NUMBER: 35186
REFERENCE/DOCKET NUMBER: S-0072.179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 210-554-5500
TELEFAX: 210-226-8395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/042,747A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
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                                                                                                                                                                                                                                                                                                                                                                                   42.1%;
ilarity 63.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2943 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 767609 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                              ; ORGANISM: Mus musculus US-09-280-799-1
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Best Local Similarity
Matches 30; Conser
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CLASSIFICATION:
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                                                                                                                                                                                                                                                         ID NO 1
FNGTH: 6727
               -09-280-799-1
Sequence 1, A
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                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08469667
Patent No. 5733748
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Yu, Guo-Liang
APPLICANT: Rosen, Craig
TITLE OF INVENTION: Colon Specific Genes and Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
                                                                                                                                                                                                     46
                                                                                                                                                                                                                  2 gctataatgcggccgcatattcggcctgatcggccgcaagcttgg
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,667
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                          16;
                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Carella, Byrne, Bain, Gilfillan, ADDRESSEE: Stewart & Olstein STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                          ed. No. 49;
Mismatches
                                                                                                                                             Score 19.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-435
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
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llarity 75.9%; Pred. No.
Conservative 1; Mismatc
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64.48;
                                         Genomic DNA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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nucleic acid
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1..501
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
              single
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nucleic acid
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                                        MOLECULE TYPE:
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US-08-469-667-1/c
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                                                                     NAME/KEY:
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LOCATION:
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US-08-042-747A-7
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                        TOPOLOGY
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Best Local S
Matches 22
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Patent No. 5925522
GENERAL INFORMATION:
APPLICANT: Wong, K.K.; Saffer, J.D.
TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of
CORRESPONDENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul W. Zimmerman
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                                                                                                                                                                                                                                       ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, ADDRESSEE: Stewart & Olstein STREET: 6 Becker Farm Road CITY: Roseland
                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Pred. No. 56;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-265
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1744
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36 CACATACACGGCCTGGTSGGCAGCCAGCT
                                                                                    PCT-US95-07289-1/c
; Sequence 1, Application PC/TUS9507289
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Rosen, Craig
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nilarity 75.9%;
Conservative
                                                                                                                                         APPLICANT: Yu, Guo-Liang
APPLICANT: Rosen, Craig
TITLE OF INVENTION: Colon
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 638 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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1..501
                                                                                                                                                                                                                                                                                                                                               ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 0 CLASSIFICATION:
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; LOCATION:
PCT-US95-07289-1
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LOCATION:
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                                                                                                                                                                                                                                                                                                              STATE:
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FILING DATE: n/a
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 8967 bases
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                                                                                                         OTHER INFORMATION:
OTHER INFORMATION:
S-08-853-659A-6
                             TYPE: nucleotide
STRANDEDNESS: dou
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                                                                                  linear
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                                                                 STRANDEDNESS
TOPOLOGY: 1
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ADDRESSEE:
ADDRESSEE:
STREET: Wa.
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US-08-853-659A-9
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Best Local S
Matches 26
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                                                                                                FEATURE
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V: A Salmonella Sequence, Methods Of Detection
V: Of A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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NO:28 correspond to nucleotides
24426 of SEQ ID NO:2
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Intellectual Property Services
Battelle Memorial Institute
PNNL P.O. Box 999
Intellectual Property Services
Battelle Memorial Institute
PNNL P.O. Box 999
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Pred. No. 78;
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                                                                                                                           3.50", 1.44 Mb
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US-08-853-659A-6/c
; Sequence 6, Application US/08853659A
; Patent No. 5925522
; GENERAL INFORMATION:
; APPLICANT: Wong, K.K.; Saffer, J.D
; TITLE OF INVENTION: A Salmonella S
; TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sec
: TITLE OF INVENTION: Salmonella Sec
                                                                                                                                                                                                                                                                                                                                       double stranded
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illarity 68.4%;
Conservative
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                                                                                                                                                                 SOFTWARE: Word Processor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08
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                            SEE: PNNL P.O. Be Washington Way Richland
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                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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APPLICATION NUMBER:
                                                                                                                                                                                                              Unknown
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APPLICATION NUMBER:
                                                                                                                                        IBM PC/XT,
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FILING DATE: Unknow
CLASSIFICATION: 435
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TOPOLOGY: lir
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Battelle Memorial Institute
PNNL P.O. Box 999
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Pred. No. 98;
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Pred. No. 98;
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nucleotides
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PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul W. Z
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Search completed: March
Job time: 5584 sec
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                                                  APPLICANT: Wong, K.K.; Saffer, J.D.
TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul W. Zimmerman
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APPLICATION NUMBER: US/08/853,659A
US-08-853-659A-64/c
; Sequence 64, Application US/08853659A
: Patent No. 5925522
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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COMPUTER READABLE FORM:
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TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
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              Sequence 64, Applicat:
Patent No. 5925522
GENERAL INFORMATION:
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SOFTWARE: Word Processor (WordPerfect 5.1)
CURRENT APPLICATION DATA:

HAPLICATION NUMBER: US/08/853,659A
FILING DATE: Unknown
CLASSIFICATION LATA:
PRIOR APPLICATION DATA:
HAPLICATION NUMBER: none
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AP001516 Bacillus
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AC068550 Homo sapi
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AL09735 Breptomy
AL109732 Streptomy
U00667 Ovis aries
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/strain="SB1003"
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/map="cosmids 143-147 of
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Submitted (07-MAY-1996) M. Fon 58th, Chicago, IL 60637, USA Location/Qualifiers
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Bacterium genome sequent
Nature 381 (6584), 653
 Similarity 80.6%; 29; Conservative
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SALALGGVAVSVGVTAAGAHYLTGLEWRQALIVGAVVSSTDAAAVFSVLRRIPLPKRI
TGTLEAESGFNDAPVVILVVAFSTAGPIEHWYVLLGEIALELAIGAAIGLAVGWLGSW
GLKHVALPASGLYPIAVMSIAIAAYAAGAMAHGSGFLAVYLASMVMGNARLPHWPATR
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GARGNRR"
856. .2007
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LARKLRLGKGDEAADLGIESAPLERLRGHLLSVTIPEGSRMHGVEVNELRLPTGAAVT
                                                                                                                                                                                                                                                                                                                                                     /translation="MPPTTTASTGQQAGTSGRKKARKGRKGRLLVLVLVLALIGGLAYGAYWSISTVRASFPQTKGSITLDGLSGPVDVKRDGYGIPQVYASTEEDLFWAQGYVQAQDRFYEMDVRRHMTAGRLSEMFGKSQIDNDEFLRTLGWHRVAKKEYDEKLSDSTKKYLQAY"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="SCE22.02, possible Na+/H+ antiporter, len: 515 aa; similar to TR:Q9XAJ9 (EMBL:AL079348) Streptomyces coelicolor putative Na(+)/H(+) antiporter SC66T3.14c, 514 aa; fasta scores: opt: 1828 z-score: 1992.7 E(): 0; 55.1% identity in 497 aa overlap. Contains Pfam match to entry PF00999 Na_H_Exchanger, Sodium/hydrogen exchanger family and possible hydrophobic membrane spanning regions"
 /note="SCE22.01c, possible secreted penicillin acylase (fragment), len: >162 aa; similar to C-terminal region of SW:PAC2_PSES3 (EMBL;M18278) Pseudomonas sp. penicillin acylase II precursor (EC 3.5.1.11) AcyII, 773 aa; fasta scores: opt: 291 z-score: 347.5 E(): 6.8e-12; 39.1% identity in 110 aa overlap. Contains possible N-terminal signal peptide sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 er integral
to TR:050532
hypothetical 41.1
                                                                                                                                                                                                                                                                                                   ylase (fragment)
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/gene="SCE22.03"
/note="SCE22.03, possible ABC transporter
                                                                                                                                                                                                                                                                                            'product="putative secreted penicillin acy
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/product="putative ABC transporter integr
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/note="nominal overlap with Streptomyces
SCE87"
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/gene="SCE22.03"
2601. .3866
'gene="SCE22.01c"
'note="SCE22.01c,
fragment), len:
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805. .2357
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/transl_table=11
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/transl_table=
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/gene="SCE22.05"
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/note="SCE22.05"
/note="SCE2.05"
/note="SCE22.05"
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LRVPGVRVLIVAFLGIGSVFGGMQVSLAAFTESIGEPGLNGVLYGVFAAGNMISGLACGAIAWKVAPQRRLLVGYAALALTASGLWAAHSVLVLAGLGLLVGMCVAPAIVTGYTLV
EDLVPAGARTEAFTWLTGAVALGQAAAVTVAGQLEDRFRDGAGFLVPMGGTVLALAVLVALRSRLATRSHGRTVARGVGHRAPATVD"
3660. .3704
/gene="SCE22.03"
/note="PS00211 ABC transporters family signature"
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                                                                                                                                                                                                                                                                                                                                               /gene="SCE22.04"
3934. .4266
/gene="SCE22.04"
3934. .4266
/gene="SCE22.04, hypothetical protein, len: 110 aa;
/note="SCE22.04, hypothetical protein len: 110 aa;
similar to TR:005574 (EMBL:Z94752) Mycobacterium
tuberculosis hypothetical 11.4 kD protein MTCI237.05c, 11
aa; fasta scores: opt: 379 z-score: 372.3 E(): 2.8e-13;
52.3% identity in 107 aa overlap. High content in serine
amino acid residue in C-terminal domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HS402G11 177241 bp DNA PRI 12-DEC-1999 Human DNA sequence from clone RP3-402G11 on chromosome 22q13.31-13.33 Contains the MAPK12 gene for mitogen activated protein kinase 12 (SAPK3), the MAPK11 gene for mitogen activated protein kinase 11 (PRKM11), gene KIAA0315, the gene for a novel protein similar to KIAA0901 and mouse histone deacetylase MHDA2, the gene for a novel protein similar to Xenopus gamma-tubulin interacting protein (yeast SPC98 homolog), the gene for a novel protein similar to yeast and bacterial predicted proteins, the genetic similar to yeast and bacterial predicted proteins, the genetic similar to yeast and bacterial predicted proteins, the genetic similar to yeast and bacterial predicted proteins.
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/gene="SCE22.05" 4397. .5239
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Pred. No. 1.9e+02
); Mismatches 1
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/transl_table=11
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                                                                                                                                                                              MAPK11; MAPK12;
ivated; MOV10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    associate primary accession
                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 29, 1999 this sequence version replaced gi:5262835.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Park Cancer
Her details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apping clones
                                                                                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was generated from part of bacterial clone contigs human chromosome 22, constructed by the Sanger Centre Chromosome Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wp:, WORMPEP; Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         corresponding to the overlapping clone, as we submit sequences widenly a small overlap as described above.

The following abbreviations are used to associate primary accessing numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP3-402G11 is from the library RPCI-3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
           the gene for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               right end of clone RP5-89814 is at 23403 in this sequence. The tright end of clone RP11-232E17 is at 56734 in this sequence. The tright end of clone RP11-232E17 is at 56734 in this sequence. The true right end of clone RP4-600024 is at 96013 in this sequence. Location/Qualifiers
                                                                             pg islands,
for a novel protein similar to C. elegans F38A5.2, the gene for novel protein similar to MRS1 and the gene for a novel protein similar to mouse MOV10 (GB110) and yeast and plant predicted proteins. Contains ESTs, GSSs and fifteen putative CpG islands,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               variations
Note that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                consensus
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                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/HGP/Chr22
During sequence assembly data is compared from overl
Where differences are found these are annotated as v
together with a note of the overlapping clone name.
variation annotation may not be found in the sequence
                                                                                                                                                                      CpG island; GB110; KIAA0315; KIAA0901; kinase; introgen activated protein kinase; mitogen-active PRKM11; SAPK3; SPC98.
                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata;
Catarrhini; Hominidae;
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..oy. .1966
/note="AluSq repeat: matches 1. .. 2504. .2574
/note="MER58 repeat: match-
2663. .2774
/note="L2 rer-
2775.
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657. .959
/note="AluSg repeat: matches 1.
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/note="AluSp repeat: matches 1.3073. .3086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="22"
                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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/clone="RP3-402G11"
/clone_lib="RPCI-3"
135. .447
                                                                                                                                                     GI:5263010
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                                                                                                     complete
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10804. .11101
/note="Alusg repeat: matches 1. .296 of consensus"
11227. .11641
/note="MER4C repeat: matches 22. .461 of consensus"
11642. .11957
/note="Alux repeat: matches 1. .310 of consensus"
11958. .11981
/note="MER4C repeat: matches 1. .22 of consensus"
14063. .14370
/note="Alux repeat: matches 2. .310 of consensus"
15488. .15718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21328. .21889
/note="MER54B repeat: matches 1. .638 of consensus"
21958. .22115
/note="L1 repeat: matches 4613. .4770 of consensus"
22116. .22245
/note="FLAM_C repeat: matches 1. .129 of consensus"
22246. .22887
/note="L1 repeat: matches 3975. .4613 of consensus"
22938. .23151
/note="FRAM repeat: matches 1. .166 of consensus"
23152. .23217
/note="L1 repeat: matches 1. .166 of consensus"
23152. .23217
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                                                                                                                                              '218. .7516
'note="AluYb8 repeat: matches 1. .318 of consensus"
    consensus
                              consensus
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                                                                                                                                ,303 of consensus"
                                                                                                                                                                                                                                                                                                                .297 of consensus"
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                                                   of
                            .527
                                                     .303
                                                                               308
/note="L2 repeat: matches 2630..2
3959..4455
/note="MER1A repeat: matches 31..
5044..5270
/note="AluJb repeat: matches 77...
6305..6592
/note="AluJo repeat: matches 29...
                                                                                        6406. .6907
/note="match: GSS: Em:AQ475194"
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23373
                                                                                                                  .853. .7155
'note="AluY repeat: matches 1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 2042)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUSGATGABA 2042 bp mRNA ROD 09-SI Mus cookii GABA transporter (GAT-1) mRNA, complete cds L32178
L32178.1 GI:533225
GABA transporter; gamma-aminobutyric acid transporter. Mus cookii (library: lambda ZAP) adult retina cDNA to reconsiderations.
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m of}
                                                                                                                                                                                                                                                                                      of
                                                                                                                                                                                                                                          31048. .31362

/note="AluY repeat: matches 1. .303 of conse

31363. .31990

/note="LiMC/D repeat: matches 4762. .5325 of

31997. .32351

/note="MLT1A1 repeat: matches 16. .365 of co

32365. .32907

/note="LiMC/D repeat: matches 4184. .4755 of

32908. .33208

/note="LiMC/D repeat: matches 1. .301 of conse

33209. .33464

/note="LiMC/D repeat: matches 3936. .4184 of

33468. .33637

/note="FRAM repeat: matches 1. .175 of conse

33650. .33707
                                                                                                                                                                  of
                                                                         .133
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/note="L1MEc repeat: matches 2231. .2

34781. .34916

/note="4 copies 34 mer 86 conserved"

34792. .34910

/note="7 copies 17 mer 73 conserved"

35157. .35466
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                 .302
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ش
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/note="L1MC/D repeat: matches 5325.31048. .31362
                               28694. .28997
/note="AluSg repeat: matches 1. .30, 29001. .29119
/note="AluJo/FLAM repeat: matches 3 29859. .30170
/note="LIME repeat: matches 5189. ..30171. .30449
/note="AluSx repeat: matches 24. .300450. .30556
/note="LIME repeat: matches 5086. ..30567. .30813
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llarity 73.2%; Pred. No. 1.4e+02.
Conservative 0; Mismatches 1:
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1. .2042
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/note="AluSg re
27926. .28225
/note="AluSx r
28694. .28997
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                            28997
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note="AluSg
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/note="AluSx
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/product="GABA transporter protein"
/product="GABA transporter protein"
/protein_id="AAA63487.1"
/db_xref="GI:204222"
/translation="MATDNSKVADGQISTEVSEAPVASDKPKTLVVKVQKKAGDLPDRDTWKGRFDFLMSCVGYAIGLGNVWRFPYLCGKNGGGAFLIPYFLTLIFAGVPLFLLECSLGQYTSIGGLGVWKLAPMFKGVGLAAAVLSFWLNIYYIVIISWAIYYLYNSFTTTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                   WKQCDNPWNTDRCFSNYSLVNTTNMTSAVVEFWERNMHQMTDGLDKPGQIRCLAITLA
IAWVLVYFCIWKGVGWTGKVVYFSATYPYIMLIILFFRGVTLPGAKEGILFYITPNFR
KLSDSEVWLDAATQIFFSYGLGLGSLIALGSYNSFHNNVYRDSIIVCCINSCTSMFAG
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IDSQFCTVEGFITALVDEYSRLLRNRRELFIAAVCIVSYLIGLSNITOGGIYVFKLFD
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GVFLFSAVQMTPLTMGSYVFPKWGQGVGWLMALSSMVLIPGYMAYMFLTLKGSLKQRL
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614 c 543 g 501 t
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M59742.1 GI:204221
GABA transporter; gamma-aminobutyric acid transporter.
Rat brain, cDNA to mRNA, clone GAT-1.
Rat tus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                  /note="gamma-aminobutyric acid transporter"
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Pred. No. 3.6e+02
; Mismatches 13
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150. .1949
/gene="GABA transporter"
/organism="Mus cookii
/db_xref="taxon:10098
/dev_stage="adult"
                                                                      /tissue_type="retina"/tissue_lib="lambda Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     type="brain"
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/gene="GAT-1"
93. .1889
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larity 68.1%;
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WKQCDNPWNTDRCFSNYSLVNTTNMTSAVVEFWERNMHQMTDGLDKPGQIRWPLAITL
AIAWVLVYFCIWKGVGWTGKVVYFSATYPYIMLIILFFRGVTLPGAKEGILFYITPNF
RKLSDSEVWLDAATQIFFSYGLGLGSLIALGSYNSFHNNVYRDSIIVCCINSCTSMFA
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LQVMIQPSEDIVRPENGPEQPQAGSSASKEAYI"
4031. .4036
/gene="GABA transporter"
1119 c 980 g 1070 t
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Liu, Z.-R., Mandiyan, S., Nelson, H. and Nelson, N. A family of genes encoding neurotransmitter transport Proc. Natl. Acad. Sci. U.S.A. 89, 6639-6643 (1992)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 4402)
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Mus musculus GABA transporter mRNA sequence
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Pred. No. 3.3e+02;
); Mismatches 15;
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                                                                                                                                                                                 DB 11;
3.3e+02;
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995 g 1077 t
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Pred. No. 3
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/product="GABA trans
1115 c 995 q
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M97512.1 GI:192680
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ilarity 68.1%;
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Chlamydia muridarum
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

(bases 1 to 10908)
Read, T.D., Brunham, R., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.
Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
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White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T.,
Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B.,
Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J.,
McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.
Direct Submission
Submitted (01-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydia muridarum, section 26 of 85 of the complete genome AE002294.1 GI:7190305
Liu,Q.-R., Mandiyan,S., Nelson,H. and Nelson,N. A family of genes encoding neurotransmitter transporters Proc. Natl. Acad. Sci. U.S.A. (1992) In press Location/Qualifiers
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241. .495
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Pred. No. 3.3e+02;
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1090 c 1230 g 1
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__41. .495
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_241. .405
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426. .1016
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                                                                                             1. 4402
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68.1%;
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QACYNESIHELKTKYRSFSKEGFGAWHSVAVSGEIGASIPIVSNGSGLFSSFSIKISA
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YSLDLGTTYRF"
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NPLFFTNNSALNGGAICCINEONLSEKGCLSLAYNOETLFSGNSAKEKGGAIYTKHMV
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IQTNTNRAVIFSSENLS
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NWTANSYIPHPERQSAL
                                                                                                                                                               TWMRLMLDSSDGKVDG
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                                                                                                                                                                                                                                                            .3707)
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8184. .9650

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Bacillus subtilis
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.

1 (bases 1 to 2013)
Henriques, A.O., Beall, B.W., Roland, K. and Moran, C.P. Jr.,
Characterization of cotJ, a sigma E-controlled operon affecting the polypeptide composition of the coat of Bacillus subtilis spores
J. Bacteriol. 177 (12), 3394-3406 (1995)
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1 426 c 553 g 519 t
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Bacillus subtilis cotJABC operon, polypeptide(s) affecting spc
coat composition, cds.
L38014
L38014.1 GI:1377748
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                                                Length 10908
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                                   DB 1; Le.
2.9e+02;
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                                               Score 23; DB Pred. No. 2.9e 0; Mismatches
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                                             48.9%;
ilarity 74.4%;
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DNA HTG 10-DEC-1999
*** SEQUENCING IN PROGRESS ***, in ordered
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E 1 (bases 1 to 17103)

S Adams, M. and Venter, J.C.

Direct Submission

L Submitted (10-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA

This sequence was identified as CDM:10211936 by the submitter. For more information on this record e-mail to fly@celera.com.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* This sequence will be preserved.

* Cocation/Qualifiers

* This sequence will be preserved.
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Bacillus subtilis strain 168 trpC2 YefA (yefA) gene, partial cds and YefB (yefB), YefC (yefC), YeeA (yeeA), YeeB (yeeB), YeeC (yeeC), YeeD (yeeD), YeeE (yeeE) and YeeF (yeeF) genes, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus subtilis.
Bacillus subtilis.
Bacillus subtilis
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.

1 (bases 15361 to 18622)
Henriques, A.O., Beall, B.W., Roland, K. and Moran, C.P. Jr.
Characterization of cotJ, a sigma E-controlled operon affecting polypeptide composition of the coat of Bacillus subtilis spores J. Bacteriol. 177 (12), 3394-3406 (1995)
95286532
2 (bases 1 to 18622)
Borriss, R. and Schroeter, R.
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 17103;
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0
    Length 2013;
                                                 Indels
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                                                                                                                     190 CCAAAATGAGGTCCAATATGCAGCATGAGCAGCCGCAAACTCTGA 146
                                                                                               47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Drosophila melanogaster"
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3705 c 3714 g 4573 t
                                                                                           3 ctataatgcggccgcatattcggcctgatcggccgcaagcttgga
                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59;
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 Score 22.6; DB Pred. No. 5e+02;
                         ed. No. 5e+(
Mismatches
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                                           0;
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AC017738.1 GI:6554261
HTG; HTGS_PHASE2.
fruit fly.
Drosophila melanogaster
                                                                                                                                                                                                                                                                                  Drosophila melanogaster,
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larity 68.9%;
Conservative (
48.18;
68.98;
                                                                                                                                                                                                                                                          17103 bp
                                               Conservative
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MEDLINE
REFERENCE
AUTHORS
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1024. .1445

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/gene="yefc"

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MTGISVSTLVRAKKKKAAEAING"
complement(1133. .1140)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lasmid PY117 orf47"
                                                                                                                                                                                                                                                                                                                                                                 Accession
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hypothetical protein MJECS02 encoded by GenBank Accession
Number L77119"
                                                                                                          Institute
    ø
                                                                                                                                                                                                                                                                                                                          /note="similar to E.coli hypothetical RNA
methyltransferase: SwissProt Accession Number P55135;
similar to Chlamydia trachomatis Homl: SwissProt Acce
Number P55137"
   chromosome,
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                                                                                                        Humboldt University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    outle="similar to Enterococcus faecalis proceded by GenBank Accession Number D78257/citation=[2]
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                                                                                                          R., Humboldt Unive
, Berlin, Germany,
segment of the Bacillus subtilis
from the purA gene cluster to the
                                                                                                                                                                                   subtilis"
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Submitted (03-JUL-1997) Borriss F
of Biology, Chausseestrasse 117,
                                                                                                                                                                                                /strain="168 trpc2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .1140)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .1129)
                                                                                                                                                            1. .18622
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                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(227.
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complement(227.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="yefB"
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                                                                                                                                                                                                                                                                                                                                                                                                    /citation=[2
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1505. .4159
  55-58 degree
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   TITLE
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LNSPVLKLIQETIDAKRINFDEDELVFIWPKV"
6064. .6069
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RCIFENGTESDMLLRSLSAELYKHGRRVTDNEDTLLDNVREDDVSTGFIYVLKSLSTD
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complement(7490. .8180)
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CDS

Number

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8277..8298
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                                                                                                                                                                                                                                                                                                                                                                                                                                         PYGTSSSGRRTPAPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEFQLDYNYDDILAS
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophila.

1 (bases 1 to 101962)

S Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hinkle,A., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Lee,B., Lewis,S., Li,P., Ling,H., Moshrefi,A.R., Moshrefi,A.R., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Richards,S., Sethi,H., Svirskas,R.R., Wan,K.H., Webster,D., Woolley,P., Yang,S., Yee,M., Yu,C. and Rubin,G.M.
                                                                                                                                                         -10.2kcal/mol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blazej, R.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to Bacillus subtilis orf94 hypothetical 59.7 kDA protein in CWLA-CISA intergenic region: Swiss Accession Number P45942"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 101962)
Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej,
Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,
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complement(9464...9470)
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complement(8308. ./gene="yeeE"
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                                                                                                                                                                                                                                            complement (8308.
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Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:6957926
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Direct Submission

Direct Submission

Submitted (08-SEP-1999) Drosophila Genome Center, Lawrence Berkeley

Laboratory, MS 64-121, Berkeley, CA 94720, USA

On Feb 11, 2000 this sequence version replaced gi:6598737.

For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (http://www.fruitfly.org/sequence/) or send email
to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet
the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 84 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
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IAVNQEQRLPIELIMDGEIIENNLKQNRLTESWLLEELRKRDIKVKETVYAVLLGNGD
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                        lognoni, A.,
Issarotti, A.,
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     emaru, K
                                                            egger,T.,
oto,K., )
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                                                                                                                                                                                                                            Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A. Direct Submission
Submitted (18-NOV-1997) I. Moszer, A. Danchin, Insti-
Regulation de l'Expression Genetique, 28 rue du Doct-
Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr,
adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax
Sorokin, A., Tacconi, E., Takagi, T., Takahashi, H., Tak
Takeuchi, M., Tamakoshi, A., Tanaka, T., Terpstra, P., T
Tosato, V., Uchiyama, S., Vandenbol, M., Vannier, F., Va
Viari, A., Wambutt, R., Wedler, E., Wedler, H., Weitzene
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Yoshida, K., Yoshikawa, H.F., Zumstein, E., Yoshikawa, H.
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Nature 390 (6657),
98044033
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Kunst, F., Ogasawara,
Direct Submission
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ACCESSION
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    Addams, M.D., Cellinker, S.E., Holl, R.A., Evalls, C.A., Goldylle, J.C., Amanatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N., Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhandy, Q., Chen, L.X., Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeiffer, B.D., Wan, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Miklos, G.L., Abril, J.F., Agbayani, A., An, H.J., Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Basu, A., Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Basu, A., Baxendale, J., Bayraktaroglu, L., Beasley, E.M., Beeson, K.Y., Berkataroglu, L., Beasley, E.M., Beeson, K.Y., Benos, P.V., Berman, B.P., Bhandari, D., Bolshakov, S., Borkova, D., Botchan, M.R., Bouck, J., Brokstein, P., Brottier, P., Burtis, K.C., Busam, D.A., Butler, H., Cadieu, E., Center, A., Chandra, I., Cadieu, E., Center, A., Chandra, I., Detz, S.M., Dodson, K., Doun, P., Durbin, K.J., Evangelista, C.C., Ferriera, S., Chandra, J., Deny, D., Dew, J., Dietz, S.M., Dodson, K., Doun, P., Durbin, K.J., Evangelista, C.C., Ferriera, S., Fleischmann, W., Fosler, C., Gabrielian, A.E., Garg, N.S., Gelbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell, J.H., Gu, Z., Gabriel, M.H., Ibeyam, C., Jalali, M., Kalush, F., Karpen, G.H., Ke, Z., Kerohim, K.A., Kimmel, B.E., Kodira, C.D., Kraft, C., Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Levitsky, A.A., Liu, X., Liu, X., Mattei, B., McIntosh, T.C., McLeod, M.P., McPherson, D., Merkulov, G., Milshina, N.V., Mobarry, C., Muzny, D.M., Noshrefi, A., Mount, S.M., Moy, M., Murphy, B., Murphy, L., Muzny, D.M., Noshrefi, A., Mount, S.M., Moy, M., Murphy, B., Murphy, L., Muzny, D.M., Palazzolo, M., Pittman, G.S., Pan, S., Pollard, J., Puri, V., Reese, M.G., Reinert, K., Remington, K.,
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Muzny,D.M., Neison,
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1 (bases 1 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evans, C.A., Gocuz..., Hoskins, R.A., Galle, R.F., ..., Henderson, S.N.,
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gene

/db\_xr <84287

;= "CG'

.>88261

xref="FLYBASE:FBgn0038935"

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JOURNAL
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FEATURES
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Zhong,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Worley
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J.S., Zhan,M
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,M., Skupski,M.P., Smith,T., Spier,E., Spradling,A.C.,
on,M., Strong,R., Sun,E., Svirskas,R., Tector,C., Turner,F.
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J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.H.,
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.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
ome sequence of Drosophila melanogaster
287 (5461), 2185-2195 (2000)
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/note="CG5732
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GAVATVAAGGAATTAVVGTSAPATGAASSSDQNVATKRNHQGAATQNNHRNRHNAKKG
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PRGLSCCGDMLNQHSEDLVFKLDQNQPDGIESGKNIFLREITEQPDNISVASNLSCSP
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Location/Qualifiers
                                                                                                                                                             HNINNAKNMTISSYSLMLMVIHFLQVGASPPVLPCLHNLYPEKFGLLQPNDFGYVDMN
EVMAPYQSDNSQTLGDLLLSFLHYYSVFDYGKYAISIRVGGVLPIEVCRAATAPKNDI
HQWNELCIEEPFDQTNTARSVYDTDTFERIKTIFVASYRRLDSTRNLSAIFEDYDGPT
                                                                                                                                                                                                                                                                SASSSKSVLAPMASKSNITMPEENNDDDELPLVVHNRYWREFFGYTPADRFLLRAKFV
EMRRPPKVMGCKNKWDPLSLSVWKKFLESQQTRHVYKIKMRLWRAIYTVAMKNYPRYG
LYLVGSSISYFGSKCSDMDICMLACTNPNIDSRMEAVYHLHVMKELLGRTNMFQDFNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YYNQTPPGINPAAVAGLTRTNRPVTQQPHILTQPAVGTTESSEEAPATLGNAPQVSST
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join(<84287. .84568,84948. .85222,85302.
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Celniker, S.E., Gibbs, R.A.,
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                                                                                >88261)
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                                                                                                    .85351,85825.
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J. Bacteri
91035268
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EIGVSFNTLVAKADEVQTLKYCVHNVADAYGKTVTFMPKPLYGDNGSGMHVHMSIAKD GKNTFAGEGYAGLSDTALYFIGGIIKHGKALNGFTNPSTNSYKRLVPGFEAPVMLAYS ARNRSASIRIPYVNSPKARRIEARFPDPSANPYLAFAALLMAGLDGIQNKIHPGDAAD KNLYDLPPEEAKEIPQVCGSLKEALEELDKGRAFLTKGGVFSDDFIDAYLELKSEEEI KVRTFVHPLEYDLYYSV"

646 c 543 g 337 t
                                                                                     /translation="MSKSLQLIKEHDVKWIDLRFTDTKGKQQHVTMPARDVDDDFFEYGKMFDGSSIAGWKGIEASDMILMPDDSTAVLDPFTEEPTLIIVCDIIEPSTMQGYDRDPRAIARRAEEYLKSTGIGDTAFFGPEPEFFIFDEVKYKSDISGSMFKIFSEQAAWNTDADFEGGNKGHRPGVKGGYFPVPPVDHDHEIRTAMCNALEEMGLKVEVHHHEVATAGQN
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/product="glutamine synthetase"
/protein_id="AAA62673.1"
/db_xref="GI:142309"
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/db_xref="ta
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/db_xref="FLYBASE:FBgn0038937"
join(98734...98776,98909...99054,99209.
100055...100449,100525...100881)
/gene="CG7086"
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'EC_number="
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46. .>1950
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/db_xref="FLYBASE:FBgn0038937"
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/db_xref="GI:7300820"
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Pred. No. 2.7e
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Search completed: March .4, 2001, 12:04:02 Job time: 5617 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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em_gss1: *
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gb_gss1: *
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193:	192:	191:	190:
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Pred. N score g and is No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

## SUMMARIES

## ALIGNMENTS

RESULT 1
AI283439/c
LOCUS
DEFINITION

ACCESSION VERSION KEYWORDS

AI283439 qh93e10. IMAGE:18 sequence AI283439 AI283439 EST. 9 9.1 9 313 bp mRNA EST 23-NOV-1998 .x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone 854570 3' similar to TR:P76904 P76904 SIMILAR TO ;, mRNA GI:3921672

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JOURNAL
MEDLINE
COMMENT
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KEYWORDS
SOURCE
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similar to
                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 520)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30;
Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                             Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA236621
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This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat.
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 313)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1854570"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                520 bp mRNA EST 07-AUG-1997
Soares_NhHMPu_S1 Homo sapiens cDNA clone TMAGE:688000
TR:G1079677 G1079677 LPE5P. ;, mRNA sequence.
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73.2%;
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Primates; Catarrhini; Hominidae;
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AI51442
                                                                                                                                                                                                     P., Lewis, S. and Rubin, C. BDGP/HHMI Drosophila EST Project Unpublished (1997)
                                                                                                             Email:
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Seq pri
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                   Univers
                                                                                                                                                                                                                                                                                                                                                                         fruit fly.
Drosophila melanogaster
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Location/Qualifiers
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This clone is available royalty-free throug
IMAGE Consortium (info@image.llnl.gov) for
Insert Length: 618 Std Error: 0.00
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                                                                                                                                             Rubin-Molecular and Cell Biology sity of California Berkeley SA, Berkeley, CA 94720-3200, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
                                                  http://www.fruitfly.org/EST,
409 row: C column: 8
mality sequence stop: 507.
Location/Qualifiers
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ewis,S. and Rubin,G.M.
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pregnant uterus"
organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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73.2%;
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                                                                                                              est@fruitfly.berkeley.edu
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                                                                                          atccaagcttgcggccgatcaggccgaatatgcggccgcattat
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BE036773
BE036773.1
EST.
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;
Caryophyllales; Aizoaceae; Mesembryanthemum.
1 (bases 1 to 1054)
Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferrea, H., Kawasaki, S., McCollough, A., Michalowski, C.B., Palacio, C.,
Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
                                                                                                                                                                                                                                                                                                                                                                                  Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513,
Tel: 520-621-7982
Fax: 520-621-1697
 AW977483
EST389592 MAGE
                                                                                                                                   31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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                                                                                                                                                                                                                                                                                                                Email: cbm@u.arizona.edu

Best blastx match: 'emb|CAB38794.1|

[Arabidopsis thaliana] 267 9e-71'.

Insert Length: 1 Std Error: 0.00.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      common ice
                                                                                                                                Similarity 70.1
31; Conservative
                                                                                                                                                                                                           /organism="Mesembryanthemum cry
/db_xref="taxon:3544"
/clone_lib="MP"
/tissue_type="apical meristem a
/dev_stage="6 weeks"
/note="3 d 500mM NaCl"
a 247 c 244 g 299 t
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/clone_lib="LD Drosophila melanogaster embryo po/
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="XL1 Blue"
/note="Organ: embryo; Vector: pOT2; Site_1: EcoR
XhoI; Sized fractionated cDNAs were directly lig.
pOT2. "
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
Brazil
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Simpson,A.J.
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                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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QV1-BT0260-281099-023-c01 BT0260 Homo sapiens cDNA, mRNA sequence.
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asimpson@ludwig.org.br
asimpson@ludwig.org.br
equence was derived from the FAPESP/LICR Human Cancer Genome
equence was derived from the following URL
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stitute for Genomic
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/db_xref="taxon:9606"
/clone_lib="MAGE resequences, |
/note="Vector: pBluescriptSKm"
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Department of Plant Pathology and Microbiology, Rm 120

Peterson Bldg, College Station, Tx 77843-2132, USA

Tel: 409 845 8743

Fax: 409 862 4790

Email: dcook@ppserver.tamu.edu

Other name: BSC-19-22; date: 6/8/99; Submitted to the D

Genome Survey Sequences (GSS) on 09/27/99; More informa

available at 'http://chrysie.tamu.edu/medicago'.

Seq primer: pUC-C
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                                                                                                                                                                                                                                                                                                                                                               Seq primer: pUC-C Class: BAC subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Cook DR
The Crop Biotechnology Center
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidao

Fabales; Fabaceae; Papilionoideae; Medicago.
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/db_xref="taxon:9606"
/clone_lib="BT0260"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

180 c 152 g 94 t 1 others
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                                                  /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="16-K-14-022"
/clone=lib="shotgun sub-library of BAC clone 16K14"
/note="Vector: pUC18; BAC survey sequences were obtained from sheared BAC DNA subcloned into the Smal site of pUC18. The template DNA for sequencing was obtained by PC purious results of the sequence of the sequenc
using universal primers. Sequencing reactions were primed from the PUC-C primer site (CAGGAAACAGCTATGACCATGATTACGA)
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clone 16-K-14-022, DNA sequence.
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VERSION KEYWORDS

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ORGANISM

ACCESSION

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W06254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: toxo@watson.wustl.edu
David Sibley at toxoest@borcim.wustl.edu for further information
relating to organism, clone or library availability.
Seq_primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hehl,A., Manger,I., Marra,M., Sibley,L.D., Ajioka,J.A., Aslett,M.A., Dietrich,N., Dubuque,T., Hillier,L., Kucaba,T., Wan,K.L., Waterston,R.H. and Boothroyd,J.
WashU-Merck-Stanford-NIH Toxoplasma EST project
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/Clone="tgzy78d04.rl"
/Clone="tgzy78d04.rl"
/Clone=lib="TgRH Tachyzoite cDNA"
/lab_host="XL1-Blue MRF'"
/note="Vector: Lambda ZAP; Site_1: EcoRI; Site_2: XhoI;
/note="Vector: Lambda ZAP; Site_1: EcoRI; Site_2: XhoI;
/note="Vector: Lambda ZAP; Site_1: EcoRI; Site_2: XhoI;
/note="Vector: Lambda ZaPI vector using the zap-cday"
foreskin fibroblast cultures in vitro. The library was
constructed by K.L. Wan, Cambridge University. cDNAs were
synthesized from polyA RNAs by oligo d(T) priming and
directionally cloned into the EcoRI to XhoI sites of the
Lambda ZapII vector using the ZAP-cDNA synthesis kit
(Stratagene). WARNING: the library contains a small
percentage of cDNAs derived from the human host cells."
36 a 66 c 78 g 83 t 3 others
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EST.
      Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma; Schizotrypanum.

1 (bases 1 to 313)

Gonzalez Rey, E., Remisz, E., Delgado Garcia, A. and Gonzal Characterization of ESTs from Trypanosoma cruzi epimasti Unpublished (1998)

Contact: Delgado Alberto
Departamento de Biologia Molecular, Lab 303

Instituto de Parasitologia y Biomedicina

Consejo Superior de Investigaciones Cientificas C/ Venta
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TENGO871
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Av. Gral Paz entre Albarellos y Constituyentes, cp(1650) San Martin, Prov. de BS AS. Argentina Tel: (54-1)752-9639 or (54-1)752-0021 Fax: (54-1)752-0021 or (54-1)752-9639 Email: dsanchez@inti.gov.ar
Seq primer: T7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 267)
Verdun, R.E., Di Paolo, N.C., Urmenyi, T.P., A.C.C. and Sanchez, D.O.
Gene discovery through expressed sequence trypanosoma cruzi
Infect. Immun. 66 (11), 5393-5398 (1998) 99003155
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Instituto de Investigaciones Biotecnologicas (Univ. San Martin)
Av. Gral Paz entre Albarellos y Constituyentes, INT
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/note="cDNA library constructed with oligente of the closed in pt7t318D modified polylinker (PHARMACIA)"
79 c 72 g 46 t 4 others
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/db_xref="taxon:5693"
/clone="1771"
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                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Toxoplasma.
                                                                                                                                                                                                                                                                            Fax: 314 286 1810
Email: toxo@watson.wustl.edu
David Sibley at toxoest@borcim.wustl.edu for further
                                                                                                                                                                                                                                                                                                                                                                                                          Unpubl
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y89b07.rl TgRH Tachyzoite cDNA Toxoplasma gondii cDNA clone
507.rl 5', mRNA sequence.
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/db_xref="ta
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/clone_lib="T. Cruzi epimastigote normalised cDNA Library"
/cell_type="epimastigote"
/note="Site_1: EcoRI; Site_2: NotI; cDNA library
constructed with oligo dt primed epimastigote mRNA and cloned in pt7t318D phagemid with modified polylinker"
91 c 83 g 67 t
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/note="Vector: Lambda ZAP; Site_1: EcoRI; Site_2: XhoI; Toxoplasma RH strain tachyzoites were grown in human foreskin fibroblast cultures in vitro. The library was constructed by K.L. Wan, Cambridge University. cDNAs were synthesized from polyA RNAs by oligo d(T) priming and directionally cloned into the EcoRI to XhoI sites of the
                                                                                                                                                                                                          ity sequence stop:
Location/Qualifiers
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/strain="Cl - Brenner"
/db_xref="taxon:5693"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:1317476
                                                                                                /clone="tgzy89b07.r1"
/clone_lib="TgRH Tachyzoite cDNA"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                  /db_xref="taxon:5811"
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AW185272
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
Putative full length read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Shoemaker R/Public Soybean EST Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sı
Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Fabales; Fabaceae; Papilionoideae; Glycine.
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se89c06.yl Gm-c1023 Glycine
Gm-c1023-1859 5' similar to
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Contact: Shoemaker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
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Shoemaker, R., Keim, P.,
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/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This cDNA library was constructed from mRNA isolated from seed coats (100-200mgs) of greenhouse grown plants. The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complimentary DNA was synthesized from mRNA using a poly (dT) sequence with a Not I restrictions site. Sal I linkers adapers were ligated to the blunt-ended cDNA fragments followed by Not I digestion. The cDNA fragments were directionally cloned into the Not I-Sal I restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells. This
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                             /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1023-1859"
/clone_lib="Gm-c1023"
                                                                                                                                                                                                                                                                    tissue_type="seed coats of greenhouse grown plants/lab_host="DH10B"
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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32-3, Kisarazu, Chiba 292-0812, Japan
asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
Location/Qualifiers
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Erika Asamizu
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                                                                                                                                                                                                                                                                                          /clone_lib="Chlamydomonas reinhardtii 5% to 0.04% CO2"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
xhoI; The cDNA library was constructed from cells cultured
in a carbon stress acclimatized condition in which carbon
dioxide concentration in the bubbling gas was changed from
5% to 0.04%"
157 c 116 g 94 t
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/clone="LC078c03_r"
                                                                                                                                                                                                                                                                                                                                                                                                            strain="C9"
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                                                  Unpublished (1998)
Contact: Dean RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson Universiy, Cl
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 40
High quality sequence stop: 464.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGTTGCGGCCGATGTAGCCGAATTCGCGGTCG
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                                                                                                                                                                                                                                                                                                                                                                                 mgxb0014023f CUGI Rice Blast BAC Library Pyricularia grisea genomic clone mgxb0014023f, DNA sequence.
AQ399560
AQ399560.1 GI:4370587
GSS.
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1 (bases 1 to 610)

Keon, J.P.R., Bailey, A.M. and Hargreaves, J.A.

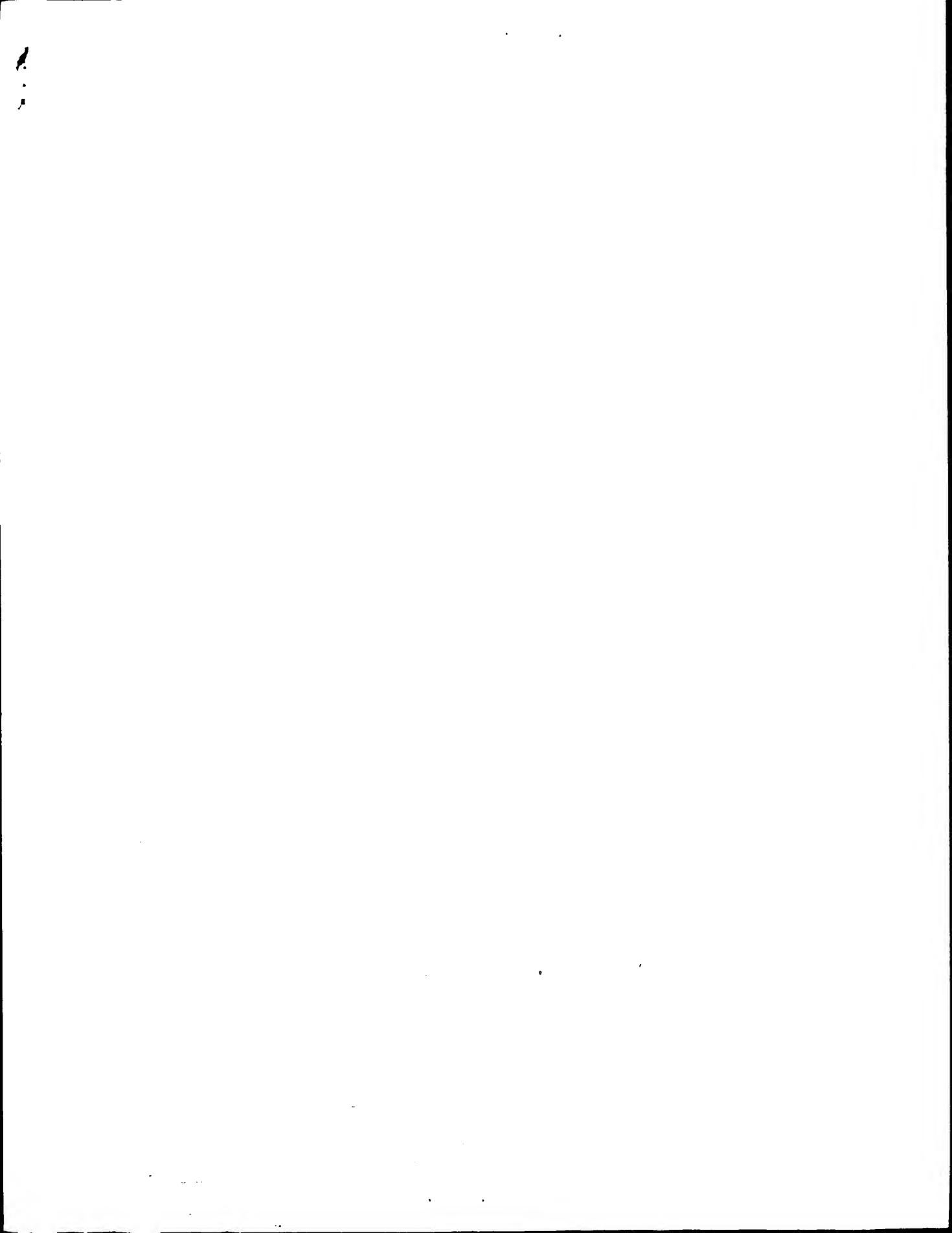
A group of expressed cDNA sequences from the blotch pathogen, Mycosphaerella graminicola
                                                                                                                                                                                                                                                               Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26;
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Eukaryota; Fungi; Ascomycota; Ascomycota incertae sedis;
                                                                                                                                                                                                                                                                                                                         Pyricularia grisea.
Pyricularia grisea
Eukaryota; Fungi; Ascomycota; Ascomycota incertae sedis;
Magnaporthaceae; anamorphic Magnaporthaceae; Pyricularia.
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/note="Vector: pSPORT1; Library constructed from cultures
utilizing ammomium ions as a source of nitrogen"
169 c 156 g 159 t 1 others
/organism="Pyricularia
/strain="70-15"
/db_xref="taxon:89476"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mycosphaerella
/strain="Strit"
/db_xref="taxon:54734"
/clone="MgA0062"
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H., Boyd,C.A.,
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                   aatccaagcttgcggccgatcaggccgaatatgcggccgca 41
 AATGCCAGCTTGGAGCCGCTCAAGGCGAAAATGGGCCAGGA 76
                                                                                          Similarity 70. 29; Conservative
                                                                                                                                                                                                                                      160
                                                                                                                                                                                                                        /clone="mgxb0014023f"
/clone_lib="CUGI Rice Blast BAC Library"
/tissue_type="Protoplasts"
/lab_host="E. coli DH108"
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25x genome coverage. High density colony filters
                                                                                                                  48.4%;
70.7%;
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Pred. No. 1.2e+02;
); Mismatches 12;
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Page 9



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1: gb_ba1:*
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11: gb_ro:*
13: gb_un:*
14: em_fun:*
15: em_hum1:*
16: em_hum2:*
17: em_in:*
18: em_om:*
20: em_ph:*
21: em_pat:*
22: em_ph:*
23: em_pl:*
24: em_ro:*
25: em_sts:*
26: em_sy:*
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31: gb_in2:*
33: gb_pl3:*
34: gb_pr4:*
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39: em_htg3:*
39: em_htg4:*
41: em_htg5:*
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## SUMMARIES

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Rhodobacter capsulatus

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69: gap of unknown length.

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20468: contig of 6240 bp in length

20468: contig of 9670 bp in length

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30338: gap of unknown length

44105: contig of 13767 bp in length

58754: contig of 14549 bp in length

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58854: gap of unknown length

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ON Human DNA sequence from clone RP3-402Gll on chromosome 22ql3.31-13.33 Contains the MAPKl2 gene for mitogen activated protein kinase 12 (SAPK3), the MAPKl1 gene for mitogen activated protein kinase 11 (PRKM11), gene KIAA0315, the gene for a novel protein similar to KIAA0901 and mouse histone deacetylase MHDA2, the gene for a novel protein (yeast SPC98 homolog), the gene for a novel protein similar to yeast and bacterial predicted proteins, the gene for a novel protein similar to C. elegans F38A5.2, the gene for a novel protein similar to MRS1 and the gene for a novel protein similar to mouse MOV10 (GB110) and yeast and plant predicted protein similar to SSSs and fifteen putative CpG islands,
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Mammalia; F
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HTG; CpG island; GB110; KIAA0315; KIAA0901; kinase; MAPK11;
MHDA2; mitogen activated protein kinase; mitogen-activated;
MRS1; PRKM11; SAPK3; SPC98.
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1 to 177241)
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/note="assembly_name:Contig22
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/note="assembly_name:Contig20"
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44206. .58754
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/db_xref="taxon:9606"
/chromosome="2"
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te="assembly_name:Contig15"
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76.38;
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Pred. No. 1.1e+02;
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entre, Hinxton, Cambridgeshire, humquery@sanger.ac.uk Clone
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5044. 50"
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3959. .4
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9427. .9542
/note="AluJo repeat: matches 30.
9543. .9847
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/note="AluSq repeat:
2504...2574
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/note="Alux repeat: matches 1.
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/note="MER58 repeat:
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/map="q13.31-13.33"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clonerequest@sanger.ac.uk
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/note="AluY repeat: matches 272. .27926. .28225
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22938. .23151
/note="FRAM r
23152. .23217
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22116. .22
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/note="Aluy
11958. .1198
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/note="Aluy
10804. .1110
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16411. .16616
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30450. .30556
/note="L1ME repeat: mainstanting and state of the color of 
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24978. .2510/
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23699. 2448
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23218. .2
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18096. .18300
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16816.
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/note="Alusg repeat:
10324. .10619
/note="Aluy 31363. .3199
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18590.
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29859. .30170
                                                                                                                                                                                                                                                                              /note="Alusx repeat: 28694. .28997
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24501. .24747
                                                                                                                                                                                                                                              /note="AluSg repeat: matches 1.
29001. .29119
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                                    /note="L1MC, 3130
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1 (bases 1 to 6254)

Schonbaum, C.P., Lee, S. and Mahowald, A.P.

The Drosophila yolkless gene encodes a vitellogenin receptor belonging to the low density lipoprotein receptor superfamily proc. Natl. Acad. Sci. U.S.A. 92 (5), 1485-1489 (1995)
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35626. .35922
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35932. .36042
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34781. .34916
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31997. .32351
/note="MLT1A1 repeat: matches
32365. .32907
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/sex="female"
/tissue_type="ovary"
/dev_stage="adult"
145. .6099
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34792. .34910
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                                                /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="gtl1 ovary cDNA library
al., Mol. Cell Biol. 9:5726(1989)"
/map="12E4-12E8; 1-48 cM"
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73.2%;
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33208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 23.4; DB 52;
Pred. No. 1.4e+02;
); Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA
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                                                                                                                                                                     schonbaum, Molecular
ty of Chicago, 920 E
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GSKEQQPLLLXTTQMTIMGMHLREDNVRNHVYQVAGNLSKVIGVAYDGSHIYWTNIQN
EAESIVKANGDGSNAEILLTSGLDAPEDLAVDWLTQNIYESDNIMRHIAVCSNDGLNC
AVLVTQDVHQPRSLAVWPQKGLMFWTDWGEKPMIGRASMDGSRSRPIVSDNIEWPNGI
ALDMHQQRIYWVDAKLGSVQTVRPDGTGRRTVLDGMLKHPYGLAIFEDQLYWSDWATK
SVHACHKFSGKDHRILAKDRTIYAVHIYHPAKQPNSPHGCENATCSHLCLLAEPEIGG
HSCACPDGMRLAPDHRRCMLMEKRQRLFIGLGQVLLEIEHTAFGAHQVSKSYTLPCLI
NEMYNRINGSLIIADNDQRLIILEFQPESHESNVLVRSNLGNVSALAFDHLSRNLYWA
DTERAVIEVLSLQTRHRALIRFFPGQEVPIGLTVMPAEGYLYVVLKAKRHSHIDKIPL
SGKGEQVHVFEDDLGDDLKLVTDYETQTIFWSDSDLGRISYSNYRVPHSQIFŘGKLR
RPYSLAMVHHDLFWNELGTPRIYWTHKSNMGPRKVIDIMEKDDPAAIMPYVPVATPNG
IPLAASSPVGQESHPCQQQNGGCSHICVGEGFYHSICLCPAGFVYRDAGNRTCVEALD
CEFRCHSGECLTMNHRCNGRRDCVDNSDEMNCDEEHRKPKVLCSPSQFACHSGEQCV
DKERRCDNRKDCHDHSDEQHCEKFDKSKKCHVHQHGCDNGKCVDSSLVCDGTNDCGDN
SDELLCEATLRCEPGMFQCGSGSCIAGSWECDGRIDCSDGSDEHDKCVHRSCPPDMHR
CLSGQCLDRSLVCDGHNDCGDKSDELNCGTDSSTMNISCAEDQNQCTSNLKICLPSAV
RCNGTTECPRGEDEADCGDVCSIYEFKCRSGRECIRREFRCDGOKDCGDGSDELSCEL
EKGHHNQSQIQPWSTSSRSCRPHLFDCQDGECVDLSRVCNNFPDCTNGHDEGPKCATA
CRSASGRQVCQHADFMLRQDRVSCKSLQSGATLLFSSFNEVRNLSEQPVMLNVAWSANDSRI
TGFDLAMHRQMGYFSAEDEGIVYQVDLQTKVIVRALELPAPTKLSVDWVTGNVYVLSG
AQEIQACSFVGRMCGRIVHVKSPRHVKHLAVDGYHARIFYIVIRTEGYGQTSSEIHMA
RLDGSRBMMT.LORSESFMTAITTTDDHOOLLVFTUDOHMBTLEBTGYGGTSSEIHMA
RLDGSRBDMT.LORSESFMTAITTTDDHOOLLVFTUDOHMBTLEBTGYGGNBDBETM
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                                                                                                                                                                                                                                                                                              /wote="iso-l (genomic DNA)"
/db_xref="FlyBase:FBgn0004649"
/replace="g"
5106
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1677 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLELEHEHEQNGHFHWLMALFVLAAGSLIAGLGYMYYQYRQRGHTDLNINMHFQNPLA
TLGGTKAFLEHERAEAGVGFTTETGTVSSRGSNDTFTTTSASSSFAAQQFSVPNALQR
LLRPRQSASGDPMAQELLLESPSRESKLHALDGGGAGGDGDGGCGVGRQVPDILVADM
DDDAAKSAGQFGGNYAGNDANARFVS."
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LQKSNALMHPSGLSVYENNAFIVNLGSMEAVQCALYGSRICHKISINVLNAQDIVVAG
RSRQPQKASHPCAHAHCHGLCLQADYGYECMCGNRLVAEGERCPHGSGNEVAVLGAVN
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NRETCLTLSEVCDGHSDCSDGSDETDLCHSKPDCDAKKCALGAKCHMMPASGAECFCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replace="a
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'db_xref="FlyBase:FBgn0004649"
'replace="a"
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/db_xref="GI:535346"
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note="yolkless"
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70.5%;
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c 1910 g
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REFERENCE
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Sequence
Unpublished
Unpublished
2 (bases 1 to 218971)
2 (bases 1 to 218971)
Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter
Celniker, S.E., Agbayani, A., Craina, T.T., Chew, M., Cic
Butenhoff, C., Champe, M., Chavez, C., Chew, M., Cic
Butenhoff, C., Champe, M., Chavez, C., Chew, M., Cic
                                                                                                                                                                                                                                                                                                                                                                                           AC01169;
HTG; HTG
                                                                                                                        Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D., Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M. Sequencing of Drosophila melanogaster
                                                                                                                                                                                                        Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra,
                                                                                                                                                                                                                                                                                                                                                                         fruit
                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster
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Drosophila melanogaster chro
12.J.5 map 12E-12E strain y;
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                                                                                                                                                                                                                                                                                                                                      Eukaryota;
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AC01510
AC01510
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This sequence was identified as CDM:10209883 by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             For
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Neoptera; Endopterygota; Diptera; Brachycera;
a; Ephydroidea; Drosophilidae; Drosophila.
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For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently

* is not known and their order in this sequence record is
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Shamanatides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galle,R.F.,
George,R.A., Lewis,S.E., Richards,S., Ashburner,M., Henderson,S.N.,
Sutton,G.G., Wortman,J.R., Yandell,M.D., Zhang,Q., Chen,L.X.,
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Kennison,J.A., Ketchum,K.A., Kimmel,B.E., Kodira,C.D., Kraft,C.,
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Adams, M.D., Celniker, S
Amanatides, P.G., Schere
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AE003495 AE002593
AE003495.2 GI:10728241
                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                        Pterygota;
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                                                                                                                                                                                                                                                                                                                                                                                fruit fly.
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1; Conservative
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183841
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176929
177629
177709
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Neoptera; Endopterygota; Diptera; Brachycera;
a; Ephydroidea; Drosophilidae; Drosophila.
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184989:
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185852:
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180601:
181263:
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y of 662 bp in lew
-brown length
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of 624 bp in le

conown length
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of 1368 bp in l
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of 511 bp in le
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of 272 bp in le
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of 572 bp
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of 248 bp
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of 841 bp
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of 497 k
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M., Henderson, S.N.,
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Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
The genome sequence of Drosophila melanogaster
L Science 287 (5461), 2185-2195 (2000)
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9, 2000 this sequence version replaced gi:7292953
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AE002294
                                                                                                                                                                                                                                                                                                         Bowman, (
                                                                                                                                                                                                                                                           Nucleic
2015025
                                                                                                                                                                                                                                                                             Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
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Read, T.D.
                                                                                                                                                                                      Bowman,
                                                                                                                                                                                                  Berry, K
                                                                                                                                                                                                           White, O.,
                                                                                                                                                                                                                        Read, T.D.,
                                                                                                                                                                           McClart
                                                                                                                                                                                                                                                                                                                               Berry,K
                                                                                                                                                                                                                                                                                                                                          White,O.,
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ydia muridarum, section 2
294 AE002160
?94.1 GT.7177
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                                                                                                                                                              Submission
                                                                                                                                                                                                                                                                       Acids
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                               /gene="TC0265"
241. .495
/gene="TC0265"
                                              /gene='
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/note="CG11585 gene product"
            putative
                                                               /note="synonym:
241. .495
/rene="TC0265"
                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                     Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J., Salzberg, S.L., Eisen, J. and Fraser, C.M.
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/db_xref="taxon:83560"
/note="synonym: Chlamydia trach
                                                                                                                                                                         Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_
                      /note="hypothetical
                                                                                                                                                                                                                                                                                                                                                                 Chlamydiales; Chlamydiaceae; Chlamydia. 1 to 10908)
                                                                                                                                                                                                                                                                                                                                                                                                   muridarum.
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codon_start=1
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70.5%;
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                                                                                                                                         Dr,
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                                                                                                                                         Rockville,
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No. 1.5e+02;
                                                                                                                                                      Institute for Genomic
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                        protein;
                                                                                                                                           MD 20850,
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                                                                                 trachomatis
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3
                         identified by
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                                                                                                                                                        Research,
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                          Glimmer2;
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                                                                                                                                                                                          Kolonay, J.,
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NPLFTNNSALNGGAICCINEQNLSEKGCLSLAYNQETLFSGNSAKEKGGAIYTKHMV
LRHNGPVSFVNNSAKLGGAIAIQSGGSLSIIAGGGSVLFQNNSCHFSDQGTVRNAIYL
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CACCUMPTETUTT COURT COU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="TC0268"
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QGFSGKQDGFEESRGEARAFADSSFTNISLPVGIAFEKKSQKTRNYYHFLGAYIQDLK
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outative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(1104 ...3707)
/gene="TC0267"
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/transl_table=11
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putative"
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426. .1016
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                                            .6192)
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CDS

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6393. KECT
                                                                                                                                                   complement(9731.
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                                                                                                         complement(9731.
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                                                                                                                                                                                                             DYMYFVEPDLPVLQITESYIDEVRQTLPELPHSKYMRYITDFDLAEDLAMILVSDRHT
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TGKIAKEIADKMVSSFGESPEDILRRHPSLLPMTDDHALRAIVKEVVAQNAASVEDYK
                                                                   Glimmer2;
                                                                                                                                                                       NGKAKALGFLVGQIMKRTEGKAPPKRVNELLLAAMRDA" complement(9731. .10834)
                                                                                                                                                                                                                                                                         MNSFTFMAQALEAEKHRQIEEYLSHPNEDPKKVVPAATYRWDPEKKKTVLMRLKERAE
                                                                                                                                                                                                                                                                                               PIVRGGCVRAIVEGEEKTFELAQTHLEDDAGMLKHFGDFAGVDYNRAGVPLIEIVSKP
CMFSAEDAVAYANALVSILSYIGISDCNMEEGSVRFDVNISVRPKGSKELRNKVEIKN
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                                                                                                                                                                                                                                                                                                                                        VCTGMPGALPVLNKDAVRKAVLFGCAVEGDVALFSRFDRKSYFYPDSPRNFQITQYEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity; putative"
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DVIAMPVCASPAIRDTDVLDPVSLYLQDIYTVAVNLAYLPAISVPSGLSKEGLPLGVQ
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6707. .8182
  /product=
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putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar
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                                                                                                                                                                                                                                                                                                                                                            translation="MGIAHTEWESVIGLEVHVELNTASKLFSPARNHFGDEPNTNISP"
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/transl_table
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Glimmer2; putative"
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/transl_table=11
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'utative; identified by match to TIGR prote
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/protein_id="AAF39138.1"
/db_xref="GI:7190310"
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Henriques, A.O., Beall, B.W., Roland, K. and Moran, C.P. Jr.
Characterization of cotJ, a sigma E-controlled operon affecting polypeptide composition of the coat of Bacillus subtilis spores J. Bacteriol. 177 (12), 3394-3406 (1995)
95286532
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519. .821
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326. 57/
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/strain="168"
/db_xref="taxon:1423"
326. .574
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PFILTGTAAGLMFSAIAVGGGAVILANPLFLMGSMTLGFALMSLHKVTYQYLSNRSQW
QKQNKIKQIESAAWENKLPKESKESSLQTSVRYSSLARKDKTRNKPGMPNKGSQVPA
SIANTERSLRSEEVLHSQSLLRQKELFPNTSNIKKELPNTKSILHTPLNRRSPSGSDS
DDVYYTPRAGLSSAETSALGDISGISSSSTSSKTSTPKAKRRVVRSSRSERNARHHRN
KEDHRQNQEESSDDEDSSPLPSPRRKKYRSRPK"
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/gene="cotJA"
/note="putative"
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836. .1405
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THPHDEDALKQFNQYSGYSRHLKRQFESSYGPLLQFGNSPAGKDWDWGKGPWPWQV"
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/gene="cotJB"
/gene="cotJC"
/note="putative"
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LFYHNAAGVPFTASYTQAKGDPIADLYEDIAAEEKARATYQWLIDISDDPDLNDSLRF
LREREIVHSMRFREAVEILKEERDKKKIF"
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                                                                                                       RGLWRQRSLVESLGGSYHQVIGDDIALVEFARAANATQLVIGVSRRGRLARRCPVRGS
VDGHRESGNIDVHIVNHAAAGGRFTLPRMAGGALTVKRRLSGLALTLILGPLITAVLV
TFRSPDSITSDVLTYQVLVVLVALVGGIWPALLAAVLSGITLDYFLVEPLFTVTVDKP
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ERATLELHGADLDASERRLLAVIAAQIDAALEHEALSVTAREVGPLAETDRVRTALLS
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                                                     VQAGVLGVTVRQVDVEDVLPRALDELGVGPDQVVLDLDAAVGPVLADPGLLQRVLVNLLANALRFSPEGAVPTIDQSFGDTVQIRVTDHGPGIAADRRDDVFVPFQRLGDTDNSTG
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/protein_id="AAB84261.1"
/db_xref="GI:2613049"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="2J"
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                                                                                                                                                                                                                                                                                                                                                                                             note="similar to E. coli sensor"
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/product="protein kinase"
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63122 St_Genes Champanelle, FRANCE
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LGLGLALSKGFTVGMGGELDTEDTPGGGLTMVVTLPVASADADANADRPGGSRASL"
771 c 931 g 475 t
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/db_xref="taxon:33887"
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/gene="DR0770"
172. .13/7
                                                             /transl_table=11
/product="hypothetical protein"
/product="hypothetical protein"
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/db_xref="GI:6458487"
/db_xref="GI:6458487"
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DTNQLRERSAALQQQIDAVAPQKSRFNDLTAQQGELERVTQVATQLRDQKTYWSNDLA
SFVERVPGNVVFSNVNMSTVAPGAEPSLAYAGKPVTRQLDLTGSARSQEAIVGFLNAF
                  AAPAPTATTPAAAPAQGGAQ"
2053. .2712
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RLAGLEPTVVDLKSFAALRALRGNLLGEHLTKSTLTGTNYTEAGEVALVMEIGASSSV
INLVRGDRILMTRNINVSADDFTTALQKAFDLDFAAAEDVKLGYATATTPTEDEEDLL
                                                         ETDSNFGVDFKGMQHDATNGIYTFTASIGVVGDQPSAAPGADPTAQGAPATGTAPAAP
                                                                                                                                                                                                                                                                         /gene="DR0771"
1340. .2056
                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAF10349.1"
/db_xref="GI:6458482"
/translation="MTSLINRFRSRSAAIGVEIGTSTIKVVALKAGAPPSLQHAVMVP
TPIGSMRDGLVVEPQAVASELKSLLAEHRITTRHAVTAVPNQVAVTRNIMVPRMDRKD
                                                                                                                                                                                                                                                                                                                                  NFDLSREQYSPARVFEVVRPVLGDLITEIRRSLEFYRVQSGDVVIDRTFLAGGGAKLR
GLAAAIGDALGFGVEVASPWLTVQTDQAGVDTGYLQTNAPEFTVPLGLALRGVMGRG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to 53.56; identified
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/chromosome="1"
172. .1347
/gene="DR0772"
                                                                                                                                                                                                                             /gene="DR0771"
/note="identified by Glimmer2; putative"
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/product="fimbrial assembly protein PilM, putative"
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/product="general secretion"
/product="general secretion"
/product="general secretion"
/product="general secretion
/product="general secretion"
/product="general
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4620. .6847
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TTTPGTTDESSGKKATGTAAKSQKGTQSGDGSDESLVATVPPLEGEGTATPPVPVPGG
INPDRPLKTLSGADPFGSLTPSPGTGTAGGTAPATPVEAQTPETQSPETAPETQAPTA
QSTTNSPAPVVLSSPAGSSVSGQGGVLDYSSRLDQGALPTPVIPVSPTEVRSPVTSAP
VSGSSVNGDSVGSGMATAPTVVVSTPAQPTTTPSASSPVARNTAGQSGAGQNTGASRP
ASGTPSRASAPNVVVVRPPPARVSGTSAAGATGSSRTGAAGTPAATPTRNQSASGTRPA
SGQTPPRVIAVAPAGGARTPAAPPAPATAAPTRPSPSSTAPSKTVVVRPPVPVSGQQ
PPRVVTSPAAGNDAAGTAALPPLITAVGSEAAPASTATADAGSSTPAAPAATALDRLLAPG
TGTAGQAGNDAAGTAALPPLITAVGSEAAPASTATADAGSSTPAAPAATALDRLLAPG
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VSLQTQGDAGTGGGGTLGSTLGLTVYTFDASGATSTPDAAAPAAGTPAPAAPAAGGTQ
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2709. .4616
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/gene="DR0774"
/note="similar to SP:Q01565 SP:P31700 G
percent identity: 48.99; identified by
similarity; putative"
/codon_start=1
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6938. .8254
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/codon_start=1
/transl_table=11
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/gene="DR0772"
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/gene="DR0773"
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                                                                                                                                                                                                                             /note="similar identified by s
/transl_table=11
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Matches 27
                                                         AUTHORS
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Bacillu
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27; Co
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Bacill
                                                     Bacillus/Staphylococcus group;
1 (bases 15361 to 18622)
Henriques, A.O., Beall, B.W., Ro
Characterization of cotJ, a sign
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8262. R077
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8965. .10017
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VPAAGVILQCVIGWVLAEAITEKFGGDTLPELQERLAAARRYAAEY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="shikimate kinase"
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EGEGYFRACEREVVQRVTRLDHAVISLGGGTFIHEENRRLLLSRGPVVVLWATPETVY
QRTKHSDRPLLKVEDPLSRIRTLMNEREGVYRQGTIHVHSDGRPSEEIVEEVVERLWA
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FVAASYLRGVAFYTAPTTLLGMVDAAVGGKTGVNLPEGKNLVGAFWPPRAVWCDTATL
TTLPDAVFREGAAEAFKHGLMADPSLLDRVVSPDFRPGGALLEDTLADAIAVKAGVVT
RDLTEQGERAFLNFGHTLAHALEAVTHQAIPHGEAVAYGMHYAARLSHALGGADLTAH
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                                                                                                           Firmicutes; Bacillus/Clostridium group; Staphylococcus group; Bacillus.
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ation of cotJ, a sigma E-controlled operon affecting composition of the coat of Bacillus subtilis spores 1. 177 (12), 3394-3406 (1995)
                                                                                                                                                                                             GI:2318058
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Borriss,R. and Schroeter,R.
The 55-58 degree segment of the Bacillus subtilis region spanning from the purA gene cluster to the
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3 (bases 1
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E 1 (bases 1 to 213190)

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299107 AL009126
299107.1 GI:2632866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAB66477.1"
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Mizuno, M., Moestl, D., Nakai, S., Noback, M., Noone, D., O'Reilly, M.,
Ogawa, K., Ogiwara, A., Oudega, B., Park, S.H., Parro, V., Pohl, T.M.,
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Yoshikawa, H. F., Zumstein, E., Yoshikawa, H. and
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68 89 4
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Nature 390 (6657), 249-256 (1997)
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Cedex 15, FRANCE. E-mail: moszer@pasteur.fr,
hin@pasteur.fr Phone: +33 (0)1 45 68 84 41, F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(755.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="ydfT"
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                                           transl_table=11
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                                                                                          to hypothetical proteins
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                                                                                           В.
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KGLAQLALQTLDERARELGAERLALHVFAHNETAVYLYQKMGYAMTNIRMRKQLC"
complement(3705. .3722)
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                                                                                                                                                                    complement (3750.
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Locus

AE004219 RESULT

KEYWORDS

VERSION

SOURCE

JOURNAL REFERENCE AUTHORS

Nature cholera

406,

477-483

(2000)

Value 100, (bases 1 to 11936)

2 (bases 1 to 11936)

Heidelberg, J.F., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.L., Heidelberg, J.F., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L.A., Dodson, R.J., Haft, D.H., Richardson, D., Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D., Gill, S.R., Nelson, K.E., Read, T.D., Bass, S., Qin, H., Dragoi, I.,

Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D. Nierman, W.C., White, O., Salzberg, S.L., Smith, H.O., Col Mekalanos, J.J., Venter, J.C. and Fraser, C.M.

JOURNAL TITLE

Direct

Submission

ted (14-JUN-2000) The I l Center Dr, Rockville,

Institute for the contract of the contract of

for Genomic

Research,

Colwell, R.R.,

USA

TITLE

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                    ACCESSION
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                                                                                                                                                                                                                                                                                            AE00421
Vibrio
Chromos
AE00421
AE00421
1 (bases 1 to 11936)
Heidelberg, J.F., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.I Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L.A., Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D., Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I., Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D., Nierman, W.C., White, O., Salzberg, S.L., Smith, H.O., Colwell, R.R., Mekalanos, J.J., Venter, J.C. and Fraser, C.M.
DNA Sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30;
                                                                                                                                                                                                                               Vibrio
                                                                                                                                                                                                                                                  Vibrio
                                                                                                                                                                                                        Bacter
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larity 69.8%;
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                                                                                                                                                                                                                            cholerae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="SWISS-PROT: P96704"
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AFVGIELVGLTAGETENPEKVIPKAINNIPVRVLLFYIGALLVIMSIYPWDIINPSES
PFVQVFVAVGIVGAASIINFVVLTSAASACNSAVFSTSRMVYSLAKDHNAPESMAKLT
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QLSGGEKLKARLAKGLSEDADLLLLDEPTNHLDEKSLQFLIQQLKHYNGTVILVSHDR
YFLDEAATKIWSLEDQTLIEFKGNYSGYMKFREKKRLTQQREYEKQQKMVERIEAQMN
GLASWSEKAHAQSTKKEGFKEYHRVKAKRTDAQIKSKQKRLEKELEKAKAEPVTPEYT
VRFSIDTTHKTGKRFLEVQNVTKAFGERTLFKNANFTIQHGEKVAIIGPNGSGKTTLL
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LGFTAAQWTEPIKHMSMGERVKIKLMAYILEEKDVLILDEPTNHLDLPSREQLEETLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_
                                                                                                                                                                                                   Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="methyl-accepting chemotaxis protein"
/protein_id="AAF94562.1"
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LANLEQDLDSLGREHEEFERKLNELLNELRSGREVKLLVADAEQIEQLQISLDQRLID
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LANEMAEGNFSKRAKVTTGDEIGQLITSMNTMAQSLSHIVGEVIDRANTIASTVTQLA
SSAESNKKSVQQQQANTEQVTSAMAQMAITITEVASSAEESSAATARAQENARYSCDV
LGKTETVSSQLVANAQQSQQMIVELEASTRQIESFVLVVEGISEQTNLLALNAAIEAA
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FSSITAAKKQLDSINLALLELTSANTQVAAASEEQSVAADEISHNMTDIRDAGETIML
SAQETAQASEELAQQAQGLKLLMGRFVIS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="VC1406"
2326. .3647
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3824. .5017
                                                                                                                                                                                                                                                                            EQTILLALNAAIEAARAGEYGRGFAVVADEVRSLASNTSQATSEIDNIVKRNSQLTEQ
SGQTMEQIQAKVTEFNHMLQQTQSLIEQIQHAAENVQKTVSNIVDE"
3824. 5017
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1. .11936
                                                                                                                                               similar to GP:3288677;
similarity; putative"
/codon start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to GB sequence similarity;
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/transl_table=
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/gene="VC1405"
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                                                                                                               /codon_start=1
/transl_table=
                                                                                                                                                                                                             3824. .5017
'gene="VC1407"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/transl_table=11
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/gene="VC1406"
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/transl_table=
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'chromosome="I"
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.220)
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:y; putative"
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GFARQAGAIRSFDLGLAASATESKVSERYQSATPPDGWNDYGTLTLNFQYDFDFWGKN
RAAVVAATSELAAAEAESVAARLMISTSIANAYAELARLYANQETVHAALQVRNKTVE
LLEKRYANGLETLGSVSQAKAVAASVEAELLGIQESIQLQKNALAALVGQGPDRAASI
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YNYFSSKEEIFTAVMESSATEQIALSFLSLDHNRELKPALLEFGYNFLNSVLTQDAMS
IYRMAIHEADRSAIGRHFYENGPKRGWARLSRYITCQIECGSLKECDPWIAAMHFKAL
LSAQYFEPFSLGAIEKPTSSELKATTQRAVEAFLCLYAAD"
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RSQAIRAQLLEDFKSGKIKYLVATGVAARGIDIDQLSRVVNYDLPFPADEYVHRIGRT
GRAEAVGEAISFVSKDNFKNLCMIESRLGHLIERRVVEGFEPKKPVPISILNYVPKHK
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8450. .9985
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                                                                                                                                                                                                                                                                      GSAFSMIPAQNATGNWIKVVQRLPIRIELDPKDLQAYPLQVGLSMVATIDTAGTTDPQ
TLVOYRAAKVSEOG"
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5785. .7239
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/gene="VC1408"
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DMGFIESINKIIDCLPSEVQFLLFSATLSRKVRELAKTAVRDPHEISIAANQASKSNI
                                                                                                                                                                                                                                                                                                          QKANAALTDNTTVDSNPEVLLAKARYEQAKIDLERTVIRAPISGIVAKRQVQVGRRVQ
VGMPLMTVVPTDHIYVDANFKEVELRDVKVGQPVTLTADLYGDDVTYHGVVAGFSGGT
                                                                                                                                                                                                                                                                                                                                                          DDTDARLALLQAEADLALAKRRVRSYLANDEGLSAMVEAQEANEQRVKAQLKAAQADF
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GGSYALYWHFIGSRYISTDNAYAAAEIAEVTPAVGGIIAQVNVVDTEYVKQGDVLVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGYQAFGLDHLFDSGNDAGAIGPAIYLPLFTGGRLEGQLTSAEARYQEAVAQYNGTLV
QALYEVADVVTSSQALQARINKTEQAVQQAEQALHIATNRYQGGLATYLDVLVAEESL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEPHITLTSRYGLPSEAGVGLLGHRADITAARWRAEAAAQQVGIAQAQFYPDVTLSAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="multidrug resistance
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                                                                                                                                                                /gene="VC1411"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="VC1409"
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                                                                                                codon_
                                                                       transl_table=11/
                                                                                                                      .larity;
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n_start=1
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                                                                                                                lar to GP:2815578; putative"
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CDS

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translation="MSHNADNEMQPLSGWALFFGALCLAMANFLAILDTTIANVSVSN

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Search completed: March Job time: 5597 sec
                                                                                                                                                                            Query Match

Best Local Similarity 73.7%;

Matches 28; Conservative
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complement(10060. .11796)
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9939. .10055
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9939.
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                  4,
                  2001,
                                                                                                                                                                         Score 22; DB 1;
Pred. No. 6.2e+02;
0; Mismatches 10
                  12:03:42
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                                                                                              6326
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4.5 Compugen Ltd.
GenCore version (c) 1993 - 2000
         Copyright
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nucleic search, using sw model OM nucleic

Search time 106.76 Seconds (without alignments) 67.930 Million cell updates/sec 4, 2001, 10:32:15; March Run on:

US-09-101-423B-7 45 Title:

score: Sequence: Perfect

.....cgaatatgcggccgcattat aatccaagcttgcggccgat.... table: Scoring

Gapext 1.0 IDENTITY\_NUC Gapop 10.0 ,

280836 seqs, 80580151 residues Searched:

56167 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed sed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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## Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES

	cripti		equence 1, App.	equence 20, App	equence 20, App	Z, Appl	I, Appl	1, Appl	10 APP	12, APP	41, APL	Segmence 3 April	o, Appl	16 APP1	יסר קקא יסר	to, Apr	L, Appl	3, Appl	o, Appi	o, Appi	ance I, Appl	12 APPL	equence 13, App	cquence // Appr	equence J, Appi	equence 1, Appr equence 10 App	cduchice io, App	equence 3, Appl	9 0	
SUMMAKIES		S-09-136-251-	-08-200-900A-2	CT-US94-00616	S-08-948-705-2	S-08-054	S-08-469-667-1	CT-US95-07289-	S-09-320-878-1	S-08-839-581A	332671-12	CT-US95-02481-	S-08-576-626A-	S-08-706-037-	S-09-005-397-1	5-09-335-409-1	5-08-278-63	5-08-403-634-3	5-08-913-44	5-08-907-229-1	-08-258-420-	3-08-850-961-1	3-08-042-747A	S-09-011-745-5	S-08-406-248-	JS94-0970	08-241-766-3	S-08-154-915-	07-970-462A	
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OF ENTEROKINASE AND METHOD OF USE

Legal Affairs

Inc.

RESULT 2
US-08-200-900A-26/c
i Sequence 26, Application US/08200900A
j Patent No. 566556
i GENERAL INFORMATION:
TITLE OF INVENTION:
CORRESPONDENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inventive:
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

Appli Appli Appli Appli Appli Appl Appl	•	60 .
88 88 88 88 88 88 88 88 88 88 88 88 88		Gaps
Sequence		th 3481; els 0;
	fri	Length
4 PCT-US92-10904-1 4 PCT-US94-09700-1 US-08-574-043A-1 2 US-08-795-015-1 4 PCT-US94-12936-1 4 PCT-US96-11886A-1 2 US-08-617-801A-3 1 US-08-920-812-22 1 US-08-920-827-22 1 US-08-920-827-22 1 US-08-920-828-22 US-08-259-148A-8 1 US-08-259-148A-8 1 US-08-259-148A-8 1 US-08-259-148A-8 1 US-08-259-148A-8 1 US-08-259-148A-8 1 US-08-259-148A-8 1 US-08-259-148A-8	ALIGNMENTS S/09136251A  LO S S S S S S S S S S S S S S S S S S	#7.1%; Score 21.2; DB 3; rity 76.5%; Pred. No. 11; nservative 0; Mismatches 8 eggccgatcaggccgaatatgcggc 37
2106 2121 2121 2121 22121 22121 69121 6914 6914 981 981	on U; Tatsi Tarc Tarc Tarc Masa} NO. D-SOR NUMBE 1997 : 9 : 9 : 9 cr. 2	47.1 76.5 vative cgatcag 
440.0 440.0 440.0 440.0 440.0 440.0 339.6 339.6	1251-1/c = 1, Application ( No. 6127156 INFORMATION: ANT: HOSHINO, Tats ANT: MIXAZAKI, Tat ANT: OJIMA, Setsuk ANT: OJIMA, Setsuk ANT: SHINJOH, Mass ANT: TOMIYAMA, NO. DF INVENTION: D-SC EFERENCE: D-Sorbit C APPLICATION NUMB C FILING DATE: 199 OF SEQ ID NOS: 9	ilarity Conservat ttgcggccga 
118 118 118 118 117 118 117 . 8 117 . 8	SULT 1 Sequence 1, Applicati Patent No. 6127156 GENERAL INFORMATION: APPLICANT: HOSHINO, APPLICANT: MIYAZAKI, APPLICANT: OJIMA, Se APPLICANT: SHINJOH, TITLE OF INVENTION: FILE REFERENCE: D-SO CURRENT APPLICATION CURRENT APPLICATION EARLIER APPLICATION EARLIER APPLICATION CURRENT FILING DATE: BARLIER FILING DATE: NUMBER OF SEQ ID NOS SOFTWARE: PATENTIN V SEQ ID NO 1 LENGTH: 3481 TYPE: DNA ORGANISM: Gluconobac	Match Local Similar Local Simi
0.000000000000000000000000000000000000	SSULT  S-09-136-29 Sequence Patent NO GENERAL IN APPLICANT APPLICANT APPLICANT APPLICANT TITLE OF FILE REFE CURRENT P COURTER P COURTER P	Query M Best Lo Matches
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APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES
TITLE OF INVENTION: TREATING COLON CANCER AND METHODS FOR DIAGNOSING AND
TITLE OF INVENTION: TREATING COLON CANCER
FILE REFERENCE: LUD-5506-JEL/NDH
CURRENT APPLICATION NUMBER: US/08/948,705A
CURRENT FILING DATE: 1997-10-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                    Gaps
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0
                                                                                                                                                                                                                                                                                                   Length 2885;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 SUBUNIT PROTEIN
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/054,077C
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Pred. No. 25;
0; Mismatches
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27-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HEMLER, MARTIN E.
APPLICANT: RAMASWAMY, HEMAVATHI
TITLE OF INVENTION: HUMAN INTEGRIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMBER: US 07/694314
01-MAY-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08054077C Patent No. 5527679 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 4093
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-5440
TELEFAX: (617) 523-6440
                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                        44.9%;
nilarity 75.8%;
Conservative (
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LENGTH: 3415 base pairs
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INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-08-948-705-2
                                                                                                                                                                                                                                                                                                                          Similarity 25; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2'CLASSIFICATION:
APPLICANT: Scanlan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                            Q ID NO 2
LENGTH: 2885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                        (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
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Pred. No. 13;
0; Mismatches
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Mismatches
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                                                                   APPLICATION NUMBER: US/08/200,900A FILING DATE: 23-FEB-1994
                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Meinert, Maureen C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI 5201-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170 X8574
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSULT 3
T-US94-00616-26/c
Sequence 26, Application PC/TUS9400616
GENERAL INFORMATION:
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71.1%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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nucleic acid
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EDNESS: single
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Best Local Similarity
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Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                      linear
                                                                                                       CLASSIFICATION:
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TOPOLOGY: 1
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US-08-054-077C-1
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Best Local Similarity 69.2%;
Matches 27; Conservative
                                            Best Loc
Matches
                                                                 Query Match
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/469,66 FILING DATE: 06-JUN-1995 CLASSIFICATION: 536
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
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                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 638 base pairs
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CITY: I
STATE:
                                          Local 51.
                                                                                                                                                NAME/KEY:
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OPERATING SYSTEM:
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TOPOLOGY: li
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                                          Similarity 75.
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& Olstein
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Pred. No.
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                                            Mismatches
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US-09-320-878-19
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PCT-US95-07289-1
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Best Local
                                                    APPLICANT: BETLACH, ME APPLICANT: McDANIEL, I APPLICANT: TANG, Li TITLE OF INVENTION: RI
                                                                                                                                                  sequence 19, Application US/09320878A Patent No. 6117659
                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 2
                                                                               APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: McDANIEL, Robert
                             CURRENT
                                          FILE REFERENCE
              CURRENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,
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ADDRESSEE: Carella, Byrne, Bandressee: Stewart & Olstein Street: 6 Becker Farm Road
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LENGTH: 638 base pairs
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CITY: 1
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LOCATION:
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ZIP: 07068-1739
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                                        OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE REFERENCE: 300622002120
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linear
ATION NUMBER: US/09/320,878A
DATE: 1999-05-27
ATION NUMBER: CIP OF 09/141,
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75.9%;
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CIP OF 09/141,908
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US-08-839-581A-21
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Best Local Sim
Matches 26;
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EARLIER APPLICATION NUMBER: CIP OF 08/84
EARLIER FILING DATE: 1997-04-30
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER FILING DATE: 1999-02-08
EARLIER APPLICATION NUMBER: 60/100,880
EARLIER FILING DATE: 1998-09-22
EARLIER APPLICATION NUMBER: 60/087,080
EARLIER APPLICATION NUMBER: 60/087,080
NUMBER OF SEQ ID NOS: 34
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SEQ ID NO 19
LENGTH: 38506
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                                                                                                                                                                                                                                    TELEFAX: 312-474-0448 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Young J. Suh
REGISTRATION NUMBER: P-41,337
REFERENCE/DOCKET NUMBER: 2786
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0,

CURRENT APPLICATION DATA:
                                                      MOLECULE TYPE:
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
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CORRESPONDENCE ADDRESS:
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                                                                                    TOPOLOGY:
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CITY: Chicago
STATE: Illinois
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FILING DATE: 1998-05-06
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                      nucleic acid
= "primer"
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PR: 27866/33886
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Sears Tower
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RESULT 10
5332671-12
; Patent No. 5332671
; Patent No. 5332671
; APPLICANT: FERRARA, NAPOLEONE; LEUI
; TITLE OF INVENTION: PRODUCTION OF
; GROWTH FACTOR AND DNA ENCODING SAME
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
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PCT-US95-02481-3/c
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5332671-12
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/38
FILING DATE: 04-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 369,424
FILING DATE: 21-JUN-1989
APPLICATION NUMBER: 351,117
FILING DATE: 12-MAY-1989
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                   APPLICATION NUMBER: 08/202,909
FILING DATE: February 28, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                             CLASSIFICATI
PRIOR APPLICAT
                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
COMPUTER: MacIntosh
                                                                                                                                                               CURRENT APPLICATION
                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS: ADDRESSEE: Jones & A
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                                                                                                                                                                                                                                                                                                                         NUMBER OF
                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                         CITY:
                                                  REGISTRATION
                                                                                                                                     FILING DATE:
                                                               NAME:
                                                                                                                                                 APPLICATION
                                                                                                                                                                        SOFTWARE:
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larity 84.0%;
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TION DATA:
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atterlee, Daniel G.
NTION: Methods of Determining the Gender of Poultry
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ousoulas, Konstantin
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                                  38,767
ER: 01051-0101
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Pred. No. 64;
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Pred. No. 60;
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US-08-576-626A-2/c
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US-08-576-626A-2
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Best Local Similarity
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                                                Matches
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Best Local Similarity
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                                                                                                                                                                                                   NAME: Dianne Casuto
REGISTRATION NUMBER: P-40,943
REFERENCE/DOCKET NUMBER: 5857
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 938-3137
TELEFAX: (847) 938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL
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                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
6190
                                                                                                                                                                                                                                                                                                  FILING DATE: 21-DEC-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE
MEDIUM TYPE: Di
COMPUTER: IBM C
                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 8051 base pair
TYPE: nucleic acid
                                                                                                                                                                                                                                                                           FILING DATE: ATTORNEY/AGENT INFORMATION:
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CITY: !
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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             tgcggccgatcaggccgaatatgcggccgcatt 43
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    Application US/08576626A
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Abbott Park
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Pred. No. 9
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                                            18.6; DB 2;
No. 1.1e+02;
6158
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RESULT 13
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INFORMATION FOR
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CORRESPONDENCE ADDRESSEE: NO
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Xu, Feng
APPLICANT: Berka, Randy M.
APPLICANT: Wahleithner, Jill A.
TITLE OF INVENTION: BLUE COPPER OXIDASE MUTANTS WITH
TITLE OF INVENTION: ENHANCED ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 30-AUG-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                       APPLICANT: Wahleith TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
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                                NUMBER OF SEQUENCES: CORRESPONDENCE ADDRE
                                                                                           APPLICANT:
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         ADDRESSEE: STREET: 4(
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REFERENCE/DOCKET NUMBER: 4526.200-US
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o. 5972670
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Berka, Randy M.
: Wahleithner, Jill A.
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Conservative
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America

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APPLICANT: Schupp, Thomas

APPLICANT: Ligon, James

APPLICANT: Ligon, James

APPLICANT: Molnar, Istvan

APPLICANT: Zirkle, Ross

APPLICANT: Cyr, Devon

APPLICANT: Goerlach, Joern

TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES

FILE REFERENCE: 4-30582A

CURRENT APPLICATION NUMBER: US/09/335,409

CURRENT FILING DATE: 1999-06-17

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 68750

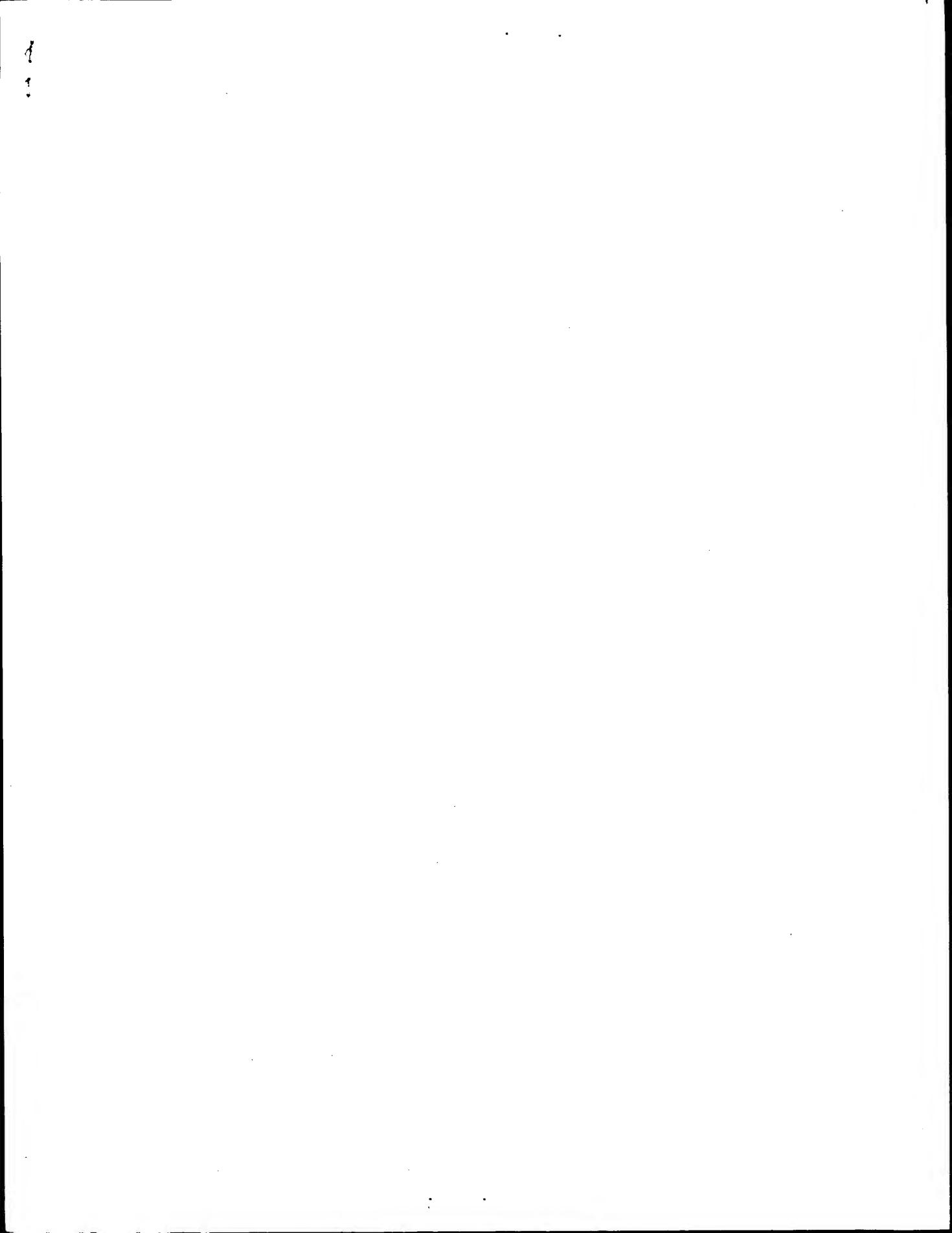
TYPE: DNA

ORGANISM: Sorangium cellulosum

US-09-335-409-1
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/706,037
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: US 60/002,800
FILING DATE: 1-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4526.200-U
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 63.6%;
Matches 28; Conservative
                                                       Query Match 40.9%;
Best Local Similarity 78.6%;
Matches 22; Conservative
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COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,397
FILING DATE:
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Matches
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The present sequence is a primer for the PCR amplification ccDNA encoding an immunoglobulin (Ig), light chain, constant The primer can be used in a novel method for the production recombinant antibodies, comprising the selection of B cells lymphocyte fraction, isolation of mRNA from individual B cel
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antibody; B cell; diagnosis; therapy;
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                                                                                                                                                                                  a
                                                                          11;
                                                                                                                                                                                                        95DE
                                                                                                                                                                                                                               95DE-1026546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38pp;
                                                                      11pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tasis-inducing DNA - used to develop products patients at risk from metastatic tumours
                                                                                                                                                                                                        -1026546
                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                           <u>;;</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                             42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English
                                                                          German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                lies - by amplification,
from B-cell mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45; DB 18; Pred. No. 7.7e-09; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>ა</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ή,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                  amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               other;
                                                                                                                                                                                                                                                                                                                                                                        region cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                             cloning
                                                                                                                                                                                                                                                                                                                                                  light
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      lls from cells,
                                                    of the
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                              0f
                                       region
                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                    chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from
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473

AATGTTCC

g

aagcttgc

Query Match Best Local S Matches 26

| Simila 26; Co

arity

47.18; 76.58;

Score 21.2; Pred. No. 14;

DB

20;

Length 500;

onservative

0;

Mismatches

8

Indels

0;

Gaps

0

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RESULT
X91235,
ID X9
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Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibodies can
method avoids t
heavy chains an
                      The invention provides isolated Toxoplasma gondii nucleic acids that encode immunogenic polypeptides. The T. gondii nucleic acid molecules, immunogenic proteins and antibodies to the proteins can be used to inhibit T. gondii oocyst shedding in a cat due to infection with T. gondii. They can be used for preventing T. gondii infection and for preventing the spread of T. gondii infection. They can also be used for detecting T. gondii infection. The detection method can be used to detect parasite cysts or oocysts in feces, e.g. from enteric apicomplexa oocysts such as Cryptosporidium oocysts and Toxoplasma oocysts.
                                                                                                                                                                                                                                                                                                                                                                                                                            Toxoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic protein; Toxoplasma gondii protein; oocyst shedding; cat;
T. gondii infection; enteric apicomplexa oocyst; Cryptosporidium oocyst;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X91235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X91235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA by
                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                  Toxoplasma gondii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-SEP-1999
                                                                                                                                                                                                                                                                                                                                                  01-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                           WO9932633-A1
                                                                                                                                                                                                                                                                                               19-DEC-1997;
                                                                                                                                                                                                                                                                                                                         18-DEC-1998;
Sequence
                                                                                                                                                                                infection caused by this microorganism
                                                                                                                                                                                           New isolated Toxoplasma gondii nucleic acids used, e.g.
                                                                                                                                                                                                                                                                     (HESK-) HESKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gondii immu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
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                                                                                                                                                                                                                                               SB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 71.0
28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription of the mRNA into cDNA, amplification of the PCR and cloning and expression of the cDNA. The recombinant ies can be used for diagnosis and/or therapy, while the avoids the need for intermediate separation of light and nains and gene library screening.
                                                                                                                                                     Page
 500
                                                                                                                                                                                                                                               Milhausen
                                                                                                                                                                                                                                                                                                                                                                                                                            oocyst; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          вP;
B₽;
                                                                                                                                                                                                                     930/35.
                                                                                                                                                       213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nogenic protein encoding DNA.
                                                                                                                                                                                                                                                                        CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         first entry)
                                                                                                                                                                                                                                                                                                 97US-0994825
                                                                                                                                                                                                                                                                                                                          98WO-US27137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 A; 11 C; 14 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
 118 A; 118 C;
                                                                                                                                                       381pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.6%;
71.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          500 BP.
                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21.4; DB Pred. No. 9.2; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                               RK;
 131 G; 133 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
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RESULT 4
X21501/c
ID X21501;
XX
AC X21501;
XX
DT 21-MAY-
XX
DE DNA seq
XX
C Sorbito
KW Sorbito
KW D-sorbi
XX
OS Glucono
XX
FH Key
FT RBS
                                                                                                                                                                                                                              WPI; 1999-134646/12.
P-PSDB; W95019, W95020.
                                                                                 13-AUG-1998;
                                                                                                                                                                                                                                                                                                                       CDS
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                                                                   21-AUG-1997;
                                                                                                24-FEB-1999
                                                                                                                                     repeat_unit
                                                                                                                                                                                repeat_region
                                                                                                                                                                                                repeat.
                                                                                                                                                                                                                                            repeat_region
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                                                                                                                                                                                                                                                                                         sig_peptide
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                                                                                                               EP897984-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gluconobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sorbitol dehydrogenase; D-sorbitol; vitamin C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X21501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAY-1999
D-sorbitol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence
                                     ,
H
                                                                                                                                                                                                _unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                    HOFFMANN
                                      Miyazaki
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f
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                                                                  97EP-0114432
                                                                                 98EP-0115231.
                                                                                                                            2803..2833
/*tag= j
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/note= "putative !
ORF2 gene
                                                                                                                                                                        2803..2892
/*tag= i
                                                                                                                                                                                                                                                                                                                                                  /note= "c
558..564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sorbitol dehydrogenase
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/note=
                                                                                                                                                                                               684..693
                                                                                                                                                                                                                                           684..704
                                                                                                                                                                                                                                                                                        572..643
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                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                     572..2794
                                                                                                                                                                                                                                                                                                                                                                                 192..572
                                                    LΑ
                                                                                                                                                                                                /*tag= e
/note= "signal
                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
177..182
                                                                                                                                                                                                                                                  /*tag= f
/note= "mature
                                                                                                                                                                                                                                                                                              /product= "SLDH gene |
/note= "corresponding
                                                                                                                                                                                                                                                                                                                     /*tag= c
/note= "putative Shine-Dalgarno
SLDH gene"
                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                  /product=
                                                                                                                                                                                                                                                                                                                                                                        *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                              *tag=
                                     Ή,
                                                   ROCHE & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                         type= inverted

"inverted repeat sequence IR2 and transcription terminator for Simulation indicated in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3481
                                                                                                                                                                                                                                                                                                                                                                                                                                                    gs
                                                                                                                                                                                                                                                                                                                                                         t= "ORF2 gene |
"corresponding
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                                                                                                                                                                                                                                                                                                              Ω
                                                                                                                                                                                                                                                                                                                                                                        b
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLDH;
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                                                                                                                                                                                                                                                                                                                                                                                     tive Shine-Dalgarno
gene"
gene
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                                                    AG
                                                                                                                                                                                                                                                   SLDH
                                                                                                                                                                                                                                                                        sequence
and
                                                    17]
                                     Shinjoh
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                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                         product"
g protein
                                                                                                                                                                                                                                                                                                      product"
recombinant
                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SLDH)
                                                                                                                                                                                                                                                                          for
                                     ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         frame;
                                                                                                                                                                                                                                                  sequence"
                                                                                                                                                                                                                                                                          SLDH"
                                                                                                                                                                                                                                                                                               sequence
                                    Tomiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                        sequence
                                                                                                                                                                                                                                                                                                                                                                                               (SD)
                                                                                                                                                                                                                                                                                                                                   (SD)
                                                                                                                                             IR2 as possible
for SLDH gene av
mation"
protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORF2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORF2
                                                                                                                                                                                                                                                                                                                                  sequence
                                                                                                                                                                                                                                                                                                                                                                                              sequence
                                     Z
                                                                                                                                                                                                                                                                                               shown in W95019"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genes
                                                                                                                                                                                                                                                                                                                                                         shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                         L-sorbose;
useful
                                                                                                                                                                                                                                                                                                                                                        in
                                                                                                                                                                                                                                                                                                                                                                                               for
                                                                                                                                                   as
                                                                                                                                                                                                                                                                                                                                                         W95020"
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g

826

aaacctgc

QУ

σ

aagcttgcggccgatcaggccgaatatgcggccgcattat 45

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12;

Indels

0;

Gaps

0;

ygctgatcaggatcaaaaggctgatgcatcat 865

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RESULT 5
V15518
ID V15518
                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
 Query Match
Best Local S
Matches 28
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This represent sorbitol dehyd reading frame needed for SLD
                                                                                                                                                                                      WPI; 199
P-PSDB;
                                                                         The present sequence is the hamster oral papilloma virus L1 DNA. The L1 protein and DNA can be used for the diagnosis of papillom virus infectious diseases related to cancer, screening for antitumour agents and antisense treatment.
                                                                                                                                                                                                                                                                                                                                                         L1 DNA; cancer;
                                                      Sequence
                                                                                                                               Claim 10; Pages 13-14; 17pp; Japanese.
                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This represents the DNA sequence of the SLDH gene encoding a protein with sorbitol dehydrogenase (SLDH) activity. The DNA also encodes an open reading frame (ORF2) product upstream of the SLDH open reading frame, needed for SLDH activity in vivo. Host cells transformed by a vector comprising the SLDH DNA sequence are used for the recombinant expression of the sorbitol dehydrogenase. Recombinant D-sorbitol dehydrogenase is useful for producing L-sorbose from D-sorbitol. L-sorbose is an important intermediate in vitamin C production.
                                                                                                                                                     DNA encoding diagnosing co
                                                                                                                                                                                                                       (TORA
                                                                                                                                                                                                                                                                   06-AUG-1996;
                                                                                                                                                                                                                                                                                        17-FEB-1998.
                                                                                                                                                                                                                                                                                                             JP10042875-A
                                                                                                                                                                                                                                                                                                                                    Hamster
                                                                                                                                                                                                                                                                                                                                                                                         Hamster
                                                                                                                                                                                                                                                                                                                                                                                                              22-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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                                                                                                                                                                                                                                             -AUG-1996;
                                                                                              present
L1 prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                      1998-1868
DB; W47224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
  Simi
28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        standa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26;
                                                                                                                                                                                                                       TORAY
                                                                                                                                                                                                                                                                                                                                    oral
                                                                                                                                                                                                                                                                                                                                                       L1 protein; diagnosis; screening; antitumour
                                                                                                                                                                                                                                                                                                                                                                                         oral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simila
26; Co
                                                        1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fig
                                                                                                                                                     ng hamster oral papilloma virus cancer related papilloma virus
 .larity 70.
                                                                                                                                                                                                                                                                                                                                    papilloma virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        rd;
                                                                                                                                                                                                                                                                                                                                                                                         papilloma virus L1 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGGCCCATGAGCATGAATACGCCGC 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gcggccgatcaggccgaatatgcggc 37
                                                                                                                                                                                                 369/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        onservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3A-D;
                                                       BP; 434 A; 346 C; 337 G; 386 T; 0 other;
                                                                                                                                                                                                                       IND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 674 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of L-sorbose, an intermediate in vitamin C production
                                                                                                                                                                                                                                             96JP-0207143.
                                                                                                                                                                                                                                                                   96JP-0207143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39pp; English.
          46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.1%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1503 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1018 C;
Score 20.8; D
Pred. No. 23;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 21.2;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                      papilloma virus agent; antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1001 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             788 T;
                      DB 19;
                                                                                                                                                     protein - useful for,
infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
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                                                                                                                                                                                                                                                                                                                                                       infectious disease;
treatment; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                      Length 1503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                              papilloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                 e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT
Z36926
ID ZZ
XX
AC Z
XX
DT 1
XX
DE N
KW P
KW P
KW S
KW S
KW S
KW S
KW S
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OS S
                                                                                                                                                                                                                                                                                                                                      RESULT
V15519
                                                                                                                                                                                                                                                                 γQ
                                                                                                                                                                                                                                               Вþ
                                                                                                                                                                                                                                                                                              Query
Best I
                                                                                                                                                                                                                                                                                      Matches
                                               Prototype Stealth virus clone; atypically structured virus; vacuolating cytopathic effect; cytopathic virus; virus detection; malignancy; multiple myeloma; lymphoma; brain tumour; breast cancer; salivary gland tumour; Alzheimer's disease; Parkinson's disease; spongiform encephalopathy; multiple sclerosis; schizophrenia; manic depression; major depression; personality disorder; autism; Rett's syndrome; attention deficit; oppositional defiance; aggression; major depression; personality disorder; autism;
                                                                                                                                                                                                                                               6474
                                                                                                                                                                                                                                                                                                                                                                 The present sequence is DNA. The DNA can be used infectious diseases related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V15519;
                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding hamster oral papilloma diagnosing cancer related papilloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP10042875-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V15519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hamster oral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosis;
                                                                                                                                                      13-MAR-2000
                                                                                                                                                                          Z36926
                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                         agents and antisense treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-186869/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-AUG-1996;
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  WO9960101-A1.
                      Stealth virus
                                         anorexia
                                                                                                                                   Nucleotide sequence
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                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                      Similarity 28; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oral papilloma virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    screening;
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                                                                                                                                                                                                                                                                                                                                      7647 BP;
                                          nervosa;
                                                                                                                                                                                                                                                                                                                                                                                                          Pages 14-16; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             papilloma virus infectious disease;
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                papilloma virus
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                                          bulimia; multi-system illness;
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                                                                                                                                   of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diseases such as a malignancy, e.g. multiple myeloma, lymphoma, brain tumours, breast cancer, salivary gland tumours, Alzheimer's disease, parkinson's disease, spongiform encephalopathy, multiple sclerosis, schizophrenia, manic depression, major depression, personality disorders, autism, Rett's syndrome, attention deficit, oppositional defiance, aggression, anorexia nervosa, bulimia, a multi-system illness, an animal illness or an illness in a domestic dog or cat. The products such as blood products and foods. The products can also be used for developing agents for treating or preventing virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention. The specification describes tissue culture, serological molecular based methods to detect atypically structured viruses, such as Stealth viruses, which are able to induce a vacuolating cytopathic effect (CPE) in tissue culture, and are distinguishable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated viruses, used to develop products and treatment of stealth virus infections
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                                                                                                                                                                                                                                                                                                                                                   6014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Martin WJ;
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 8929
                                                                                         Location/Qualifiers
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           "this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"
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                                                                                                      invention relates to a method of detecting and characterising a stealth virus by reacting a sample suspected of containing a stealth virus with a robe from a known stealth virus and sequencing the resultant isolated nucleotide. The method comprises the steps of: (a) isolating DNA or RNA cells showing a viral cytopathic effect; (b) testing the reactivity of the isolated DNA or RNA with a molecular probe that contains at least 18 cor more contiguous nucleotides identical to sequence previously identified from a stealth virus; and, optionally (c) sequencing the isolated DNA or RNA molecules that react with the probe. The method is clearly contained to detect stealth virus in a biological product, food or in the movironment. The method is also used to evaluate agents for their inhibitory or stimulatory effects on stealth virus replication and to determine capacity of the virus to recombine with and potentially alter the nucleic acid sequences of a cell or bacterium.
                        Query Match
Best Local S
Matches 25
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caagettgeggeegateaggeegaatatgeggee
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                   25; Conservative
                                                                                     9181 BP;
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Pred. No. 28;
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PD 21-JUL-
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PF 13-JAN-
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PF 15-JAN-
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RESULT
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Z29251
                                                                                                                                                                                                                                                                                                          Nested oligonucleotide primers were synthesised which were complementary to the lambda DNA sequence adjacent to the cloning site for the cDNA insertions (see Q70113-14). In addition, primers were designed which were complementary to the plus strand of the most 5' region of the EK coding sequence (see Q70115-16). Subcloning and sequencing provided a 116 amino acid EK heavy chain. This protein contained regions corresp. to tryptic peptides (see R57295-9).
                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding enterokinase activity - and related vectors, host cells, expression products and antibodies are useful in treating digestive disorders and for cleaving fusion
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71.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B₽.
                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                     Score 20.4;
Pred. No. 22;
                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6053
                                                                                                                                                                                                                                                  DB 15;
                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                Length 41;
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                       Gaps
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0;

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Query Match
Best Local
Matches 2
                                                                                                                                                                                                                              83
                                                                                                                                                                                                                                                                                                                                                                         were used to characterise the protein expression from various life cycle stages of P.falciparum. Oligonucleotide primers were used to amplify each selected ORF from chromosome 2 using genomic DNA as template. The purified amplified products were cloned into the mammalian expression plasmid VR1050 to produce DNA vaccines for immunisation. Blood and sera obtained from groups of mice immunised with doses of vaccine was used to identify stage specific expression of Rifin protein by immunofluorescent antibody testing. The method is useful for determination of subcellular localisation of proteins and for the development of antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use
of v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stage specific protein expression; antimicrobial vaccine;
antimicrobial drug; IAF; immunofluorescent antibody testing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USNA
                                     CDS
                                                                           Key
CDS
                                                                                                                            Diagnosis;
                                                                                                                                              Sequence encoding proteins.
                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hoffman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-APR-1998;
23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9955381-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum
                                                                                                        Mycobacterium
                                                                                                                                                                                                                   N81768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-APR-1999;
                                                                                                                                                                             29-DEC-1990
                                                                                                                                                                                                                                                                    702
                                                                                                                                                                                                                                     11
                                                                                                                                                                                                                                                                                                                             Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine,
                                                                                                                                                                                                                                                                                      N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of microbial,
                                                                                                                                                                                                                                                                2000-086380/07
                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                        similarity 71.1%;
27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SL,
                                                                                                                                                                                                                                                                                                                                                          939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 16; 23pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEC
                                                                                                                           assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 obial, animal and/or drug or diagnostic p
                                                                                                                                                                                                                                                                                                                                                         ВP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carucci
                                                                                                                                                                            (first
                                                                                                        tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF.
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99US-0082947
                                            252..1874

/*tag= a

/label=540 AA protein

/note="p81351"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US09047
                /*tag= b
/label=517
                                                                                                                                                                                                                                                                                                                                                          365
                                                                                    Location/Qualifiers
                                                                                                                                                                                                                   DNA; 4260 BP
/note="P81868"
                                   complement (3948..2395)
                                                                                                                           M.bovis;
                                                                                                                                                         Mycobacterium
                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                         Α,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the Rifin
                                                                                                                                                                                                                                                                                                                                                          133
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                                                                                                                            vaccine;
                                                                                                                                                                                                                                                                                                                                                         C;
                                                                                                                                                                                                                                                                                                        Score 20.4; Depred. No. 31; O; Mismatches
                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                         172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human genomic
                                                                                                                                                          tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3193 gene of chromosome
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                                                                                                                            ds
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                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                       39
                                                                                                                                                          540
                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            data
                                                                                                                                                                                                                                                                                                                                                          other;
                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                          517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identification
                                                                                                                                                                                                                                                                                                                            939;
                                                                                                                                                          A
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                                                                                                                                                          residue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rifin
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes
                                                                                                                                                                                                                                                                                                          0,
                                                       g
                                                                                                                                                                                                                                                         N80222/c
ID N80222
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
Matches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 198
P-PSDB;
                                                                                                                  Key
CDS
                                              11-AUG-1988
                                                                  W08805823-A
                                                                                               CDS
                                                                                                                                                                  Antigen;
                                                                                                                                                                                     protein.
                                                                                                                                                                                                                   19-MAR-1991
                                                                                                                                                                                                                                       N80222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shinnick T,
                                                                                                                                                                                                                                                                                                                            12
                                                                                                                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                  Match
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$\times CCCCCCCCX\times \times \times
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An isolated DNA molecule that consists essentially of the nucleotide sequence that corresponds to the sequence represented by position 3950 to about 2390 and from position 3948 through position 2398 of N81768 is claimed. Also claimed is a peptide sequence that consists of a 5-40 AA residue sequence that corresponds to a sequence of the 540 AA residue protein (P81351) or the 517 AA residue protein (P81868) coded for by the DNA sequence. The proteins can be used for determining previous immunological exposure of a mammal to M.tuberculosis or M.bovis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant mycobacterial peptide(s) - used in assays for diagnosis of infection, vaccines and for producing antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-FEB-1988;
06-FEB-1987;
02-FEB-1987;
                                                           01-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO8806591-A.
                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunologica
for producin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1988-271;
3DB; P8135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standa:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCRIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vacc:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     щ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>_</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ycobacterium tuberculosis DNA contg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rd;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  onservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 733 A; 1332 C; 1481 G; 714 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                             tuberculosis.
87US-0010007.
                                                              88WO-US00281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87US-0019529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88US-0159667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88WO-US00598.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLINIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P81868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2a-2d; 116pp;
                                                                                                                                                                                                           /*tag= a
complement (2398..4101)
/*tag= b
                                                                                                                                                                                                                                                                                                                                    192..1874
                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA; 4380 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.3%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20.4; D
Pred. No. 37;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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CE CONTROL OF CONTROL 
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V05708/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 24
                                                                                            WPI; 199
P-PSDB;
          autoantigen-coated particles or construct
                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heat
gene
                                                                                                                                                       Haynes
                                                                                                                                                                                                                              03-JUN-1997;
03-JUN-1996;
                                                                                                                                                                                                                                                                                       03-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3630
                                                                                                                                                                                         (AURA-) AURAGEN INC
                                                                                                                                                                                                                                                                                                                              11-DEC-1997.
                                                                                                                                                                                                                                                                                                                                                                   W09746253-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V05708 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The gene was isolated by probing a lambda gtll expression library of M.tuberculosis DNA with monoclonal antibodies directed against M.tuberculosis-specific antigens. The 19kD, 71kD and the 65kD proteins and genes are claimed, and so is a vaccine comprising DNA encoding M.tuberculosis protein in a recombinant vaccine vector. P80216 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 190
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V05708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4380 BP; 757 A; 1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genes encoding Mycobacterium to useful for developing reagents treatment of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoded on the complementary strand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Fig 8; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (WHIT-) WHITEHEAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13
                                                                                            1998-041892/04
DB; W44702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  shock protein;
therapy; rheum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1988-235175/33.
DB; P80215, P80216
                                                                                                                                                   JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 80. 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RN,
                                                                                                                                                 Prayaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tuberculosis
                                                                                                                                                                                                                             97US-0019100
96US-0019100
                                                                                                                                                                                                                                                                                      97WO-US09427.
                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/product=
                                                                                                                                                                                                                                                                                                                                                                                                                       252..1874
/*tag=_a
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA; 4380 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RΑ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Μt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                   SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.3%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hsp65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shinnick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arthritis;
                                                                                                                                                  Ramshaw
                                                                                                                                                                                                                                                                                                                                                                                                        65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                       kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tuberculosis protein antigens - ts for diagnosis, prevention and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ű
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kDa heat
                              autoantigen-encoding
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                                                                                                                                                                                                                                                                                                                                                                                                       heat
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No. 37;
                                               by administerin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3601
                                                                                                                                                                                                                                                                                                                                                                                                   shock protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              shock protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ŧ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunotherapy;
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                               nucleic
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                               acid
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RESULT Z46842/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This DNA sequence encodes the 65 kDa heat shock protein (see C W44702), designated Mt Hsp65, of Mycobacterium tuberculosis. This protein cross-reacts with a component of articular cartilage, human the component of articular cartilage, human collaboration in a claimed method for treating or preventing an autoimmune disease in a mammal comprises: (a) providing a particle coated with an antigen cagainst which an immune response is mounted in the autoimmune response is construct components in the recipient cell of the construct components of the components of a reduction in a cottocoxic and construct components of a coding sequence for the contigen, operably linked to control elements such that the coding sequence can be transcribed and translated in a recipient cell, and cellivering the construct to the recipient cell using a gene gun. The antigen of step (a) is selected from collagen, Mt Hsp65, myelin basic protein, myelin oligodendrocyte glycoprotein, cytotoxic responses and elicit antigen desensitisation. The method is used especially for treating rheumatoid arthritis or multiple sclerosis. It represents a novel use for the known Mt Hsp65 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
                                                                                Disclosure;
                                                                                                                           New semaphorin
                                                                                                                                                                                                                                      11-MAR-1998;
                                                                                                                                                                                                                                                                   11-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                               Unidentified.
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                                                                                                                                                           P-PSDB;
                                                                                                                                                                                                                                                                                                  14-DEC-1999.
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                                                                                                            immunogens
                                                                                                                                                                                                       (EXEL-) EXELIXIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                            immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Semaphorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Z46842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z46842
                                                                                                                                                                                                                                                                                                                                                                                                           Semaphorin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                          K1; cellular physiology; neurite outgrowth; neuron;
pharmaceutical; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>~</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 55-59; 72pp; English.
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                                                                            ige 17-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        gene related sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP; 757 A; 1371 C;
                                                                                                                       polypeptides, useful cell physiology modulators
                                                                                                                                                                                                                                      98US-0041236
                                                                                                                                                                                                                                                                    99ЛР-0065672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.3%; Score 20.4;
80.0%; Pred. No. 37;
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                                                                            57pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B₽.
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                                                                                                                                                                                                                                                                                                                                                                                                         human;
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The invention polypeptides, cellular physi

lular physic polypeptide

or nucleic acids encoding them, can be used to miclogy by modulating semaphorin K1 activity, e.g. e fragments or antisense nucleic acids can be use

provided isolated human semaphorin K1 polypeptides.

to modulate

semaphorin

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Best Loc
Matches
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17-JUL-1997;
10-OCT-1997;
10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enhance neurite outgrowth from damaged neurons. The polypeptides can also be used as immunogens, reagents for isolating other semaphorins, or as reagents for screening chemical libraries for lead pharmaceutical agents. The nucleic acids can also be used as probes and primers for diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cancer
breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X40055;
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The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast
                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Colon cancer associated gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prostate
                                                                                                                                                                    Claim 67; Page 651-652; 787pp;
                                                                                                                                                                                          New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                        Tureci 0;
                                                                                                                                                                                                                                                                                                Chen Y,
                                                                                                                                                                                                                                                                                                                       (LUDW-) LUDWIG
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                                                                                                                                                                                                                                               1999-132448/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    associated antigen; diagnosis; research; treatment;
cancer; colon cancer; gastric cancer; renal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   th 44.9%; Similarity 68.3%; 28; Conservative
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                                                                                                                                                                                                                                                                                                Gout
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Scanlan
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Pred.
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                                                                                                                                                                    English.
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                                                                                                                                                                                                                                                                                      Obata Y, ', Stockert
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SQ XX
               cancer, rendern lung cancer
Sequence 2885
                       renal
ВP;
                        cancer, colon cancer, gastric cancer, prostate cancer
 626 A;
 901 C;
 838 G;
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  other;
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                             Query Match
Best Local S
Matches 25
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24.9%; Similarity 75.8%; 25; Conservative
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Pred. No. 43;
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